

GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Cheever, Martin A.
APPLICANT: Hand-Zimmerman, Susan
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
TITLE OF INVENTION: AND VIRUS-ASSOCIATED MALIGNANCIES
FILE REFERENCE: 210121.483C3
CURRENT APPLICATION NUMBER: US/10/313,644
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-313-644-3

Query Match 100.0%; Score 54; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVLVPOQGF 10
Db 1 EEVLVPOQGF 10

RESULT 3
US-09-854-356-5

Sequence 5, Application US/09854356
Patent No. US20020177567A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Gheyssen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins
FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 59
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: fragment of the phosphorylation domain, preferred
OTHER INFORMATION: portion (delta PD) of human HER-2/neu
US-09-854-356-5

Query Match 100.0%; Score 54; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVLVPOQGF 10
Db 32 EEVLVPOQGF 41

RESULT 4
US-09-854-356-4

Sequence 4, Application US/09854356
Patent No. US20020177567A1
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Gheyssen, Dirk
APPLICANT: Corixa Corporation
APPLICANT: SmithKline Beecham Biologicals S. A.
TITLE OF INVENTION: HER-2/neu Fusion Proteins

FILE REFERENCE: 014058-009810PC
CURRENT APPLICATION NUMBER: US/09/854,356
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: US 09/493,480
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,976
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 266
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: phosphorylation domain (PD) of human HER-2/neu
US-09-854-356-4

Query Match 100.0%; Score 54; DB 10; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVLVPOQGF 10
Db 32 EEVLVPOQGF 41

RESULT 5
US-10-102-806-583

Sequence 583, Application US/10102806
Publication No. US2003005442A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 583
LENGTH: 293
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (53)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (150)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (58)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (171)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (207)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (254)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-102-806-583

Query Match 100.0%; Score 54; DB 15; Length 293;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 7, 2004, 13:26:19 ; Search time 11 Seconds
(without alignments)
42.752 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 54

Sequence: 1 EBYLVPOQGF 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	245	1 ERB2_MOUSE	P70424 mus musculu
2	54	100.0	1254	1 ERB2_MOUSE	O60553 mesocricetu
3	54	100.0	1255	1 ERB2_HUMAN	P04628 homo sapien
4	54	100.0	1257	1 ERB2_RAT	P06494 rattus norv
5	50	92.6	1210	1 EGFR_HUMAN	P00533 homo sapien
6	50	92.6	1210	1 EGFR_MOUSE	Q01279 mus musculu
7	46	85.2	548	1 ERBB_AVIEU	P11273 avian eryth
8	46	85.2	604	1 ERBB_AVIER	P00535 avian eryth
9	46	85.2	634	1 ERBB_AVY	P00534 avian leuko
10	38	70.4	232	1 YH73_SYNY3	P73623 synechocyst
11	37	68.5	95	1 ERB4_MOUSE	O61527 mus musculu
12	37	68.5	687	1 TGM2_BOVIN	P51176 bos taurus
13	37	68.5	687	1 TGM2_HUMAN	P08587 homo sapien
14	37	68.5	689	1 TGM2_CANCU	P08588 cavia crite
15	37	68.5	1308	1 ERBB_HUMAN	Q15303 homo sapien
16	37	68.5	1308	1 ERBB_RAT	O62956 rattus norv
17	36	66.7	541	1 FTCD_HUMAN	O09954 h. foetimid
18	35	64.8	391	1 TGM2_MOUSE	P39101 saccharomyc
19	35	64.8	686	1 TGM2_MOUSE	P11981 mus musculu
20	35	64.8	917	1 NIA2_ARA.TH	P11035 arabidopsis
21	35	64.8	1242	1 MSH6_YEAST	Q03874 saccharomyc
22	35	64.8	2269	1 WDR9_HUMAN	Q09146 homo sapien
23	34	63.0	262	1 YES9_HELPT	O61590 helicobacte
24	34	63.0	364	1 MURG_THETN	O61956 thermococ
25	34	63.0	365	1 MURG_SHEVI	O61956 thermococ
26	34	63.0	474	1 SYE_EUCAP	O61956 thermococ
27	34	63.0	541	1 FTCD_PIG	O61956 thermococ
28	34	63.0	598	1 NUSM_PETMA	O35543 petromyzon
29	34	63.0	988	1 TNP2_ECOLI	P06694 escherichia
30	34	63.0	997	1 Y414_MYCPN	P75183 mycoplasma
31	34	63.0	1097	1 TOLL_DROME	P08953 drosophila
32	34	63.0	2290	1 POLG_EMCV	P03304 encephalomy
33	34	63.0	2292	1 POLG_EMCVB	P17593 encephalomy

ALIGNMENTS

34	34	63.0	2292	1	POLG_EMCVD	P17594 encephalomy
35	35	61.1	262	1	YES9_HELPT	P55986 helicobacte
36	33	61.1	370	1	MYOM_APLCA	P15513 a myomodul
37	33	61.1	390	1	NCF1_MOUSE	O09014 mus musculu
38	33	61.1	392	1	YAV1_SCHPO	O10209 schizosacch
39	33	61.1	439	1	LIP1_DROME	O46107 drosophila
40	33	61.1	459	1	T7L2_MOUSE	O97480 mus musculu
41	33	61.1	541	1	FTCD_MOUSE	O91484 m foetimid
42	33	61.1	541	1	FTCD_RAT	O88618 r foetimid
43	33	61.1	584	1	T7L1_MOUSE	O92131 mus musculu
44	33	61.1	588	1	T7L1_HUMAN	O91954 homo sapien
45	33	61.1	619	1	T7L2_HUMAN	O91954 homo sapien

RESULT 1
ID ERB2_MOUSE STANDARD; PRT; 245 AA.
AC P70424; Q61525;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Receptor (protein-tyrosine kinase erbB-2 (BC 2.7.1.112) (p185erbB2)
DE (NEU proto-oncogene) (C-erbB-2) (fragments).
GN ERBB2 OR NEU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE OF 1-149 FROM N.A.
RC STRAIN=CD-1; TISSUE=Uterus;
RX MEDLINE=97200814; Pubmed=9048643;
RA Lipp J., Day S.K., Das S.K.;
RT "mouse uterus: potential mediator of signaling by epidermal growth
RT factor-like growth factors.";
RT Endocrinology 138:1328-1337(1997).
RN [2]
RP SEQUENCE OF 150-245 FROM N.A.
RX MEDLINE=96069911; Pubmed=7589796;
RA Kobosco L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P.,
RA Sanes J.R.;
RT "Synapse-associated expression of an acetylcholine receptor-inducing
RT protein, ARIA/herculin, and its putative receptors, ErbB2 and ErbB3,
RT in developing mammalian muscle.";
RL Dev. Biol. 172:158-169(1995).
RN [3]
RP INTERACTION WITH PRKCAP.
RX MEDLINE=2126773; Pubmed=11278603;
RA Jaulin-Bastard F., Saito H., Le Bivic A., Ollendorff V., Marchetto S.,
RA Bribaud D., Borg J.-P.;
RT "The ERBB2/HER2 receptor differentially interacts with ERBIN and PICK1
RT PSD-95/Dlg-2/-1 domain proteins.";
RL J. Biol. Chem. 276:15256-15263(2001).
CC -1- FUNCTION: Essential component of a neuroligin-receptor complex,
CC although neuroligins do not interact with it alone. Gp30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha and amphiregulin.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC (potential). Interacts with PRKCAP.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Expressed predominantly in uterine epithelial
CC cells. In the muscle, expression localizes to the synaptic sites
CC of muscle fibers.
CC -1- DEVELOPMENTAL STAGE: On days 1-4 of pregnancy, ERBB2 is detected
CC primarily in epithelial cells, the day 1 uterus showing the
CC highest accumulation. On day 5, the epithelium and the
CC decidualizing stromal cells around the implanting blastocyst

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CC exhibit accumulation of this receptor. On days 6-8, the expression
CC persists in the epithelium at both the implantation and
CC interimplantation sites in addition to modest levels in the
CC secondary decidual zone. On days 7 and 8, accumulation is also
CC prominent in the trophoblastic giant cells.
CC -1- PIV: Ligand-binding increases phosphorylation on tyrosine
CC residues (By similarity).
CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See license@isb-sdb.ch).
CC -----
CC DR EMBL: U71126; AAB17380.1; -.
CC DR EMBL: L47239; AAA93532.1; -.
CC DR HSSP: P11362; 1P6K.
CC DR MGD; MGI:95410; EtDb2.
CC DR GO; GO:0007507; P:heart development; IMP.
CC DR GO; GO:0007422; P:peripheral nervous system development; IMP.
CC DR InterPro: IPR000719; Prot kinase.
CC DR InterPro: IPR001245; Tyr kinase.
CC DR PRINTS: PR00109; TYRKINASE.
CC DR ProDom: PD000001; Prot_kinase; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; PARTIAL.
CC DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
CC DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC DR Transmembrane; Glycoprotein; Mulfegene family; Receptor; Transferase;
CC KM Tyrosine-protein kinase; ATP-binding; Phosphorylation.
CC FT NON_TER 1 1
CC FT DOMAIN <1 >149 PROTEIN KINASE.
CC FT ACT SITE 61 61 BY SIMILARITY.
CC FT NON_CONS 149 150
CC FT NON_TER 245 245
CC SQ SEQUENCE 245 AA; 26927 MW; 0F763F0363DFEFC CRC64;

OY Query Match 100.0%; Score 54; DB 1; Length 245;
Db Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EBYLVPOQGF 10
Db 160 EBYLVPOQGF 169

RESULT 2
ERB2_MESAU STANDARD; PRT; 1254 AA.
AC 060553;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)
DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2).
GN ERBB2 OR NEU.
OS Mesocricetus auratus (Golden hamster).
OS Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxId=10036;
RN [1] _
RP SEQUENCE FROM N.A.
RC TISSUE=Nerve;
RX MEDLINE=94193007; PubMed=7908275;
RA Nakamura T., Uehijima T., Ishizaka Y., Nagao M., Arai M.,
RA Yamazaki Y., Ishikawa T.;
RT "Cloning and activation of the Syrian hamster neu proto-oncogene.";
RL Gene 140:251-255(1994)
CC -1- FUNCTION: Essential component of a neuroguilin-receptor complex,
CC although neuroguilin do not interact with it alone. GP30 is a

```

CC	potential ligand for this receptor. Not activated by EGF, TGF-
CC	alpha and amphiregulin (By similarity).
CC	-1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC	tyrosine phosphatase.
CC	-1- SUBUNIT: Heterodimer with each of the other ERBB receptors
CC	(potential). Interacts with PRKCA/B (By similarity).
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- PTM: ligand-binding increases phosphorylation on tyrosine
CC	residues.
CC	-1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	use by non-profit institutions as long as its content is in no way
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL, D16295, BAA03801.1, -.
DR	PIR, I48161, I48161.
DR	HSSP, P11362, IFGK.
DR	InterPro, IPR000494; EGFR_L_domain.
DR	InterPro, IPR006211; Furin-like.
DR	InterPro, IPR006212; Furin repeat.
DR	InterPro, IPR000719; Prot_Kinase.
DR	InterPro, IPR001245; Tyr_PKinase.
DR	InterPro, IPR004019; YLP motif.
DR	Pfam, PF00757; Furin-like, 1.
DR	Pfam, PF00069; pkinase; 1.
DR	Pfam, PF01030; Recep_L_domain; 2.
DR	Pfam, PF02757; YLP_2.
DR	PRINTS, PR00109; TYRKINASE.
DR	PRINTS, PD000001; Prot_Kinase; 1.
DR	SMART, SMO0261; FU, 4.
DR	SMART, SMO0219; TYRK; 1.
DR	PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
DR	PROSITE, PS50011; PROTEIN_KINASE_DOM; 1.
KW	Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
KW	transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
KW	Proto-oncogene; Disease mutation.
FT	SIGNAL 1 21 POTENTIAL.
FT	CHAIN 22 1234 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
FT	DOMAIN 22 652 EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM 653 675 POTENTIAL.
FT	DOMAIN 676 1254 CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 158 368 CYS-RICH.
FT	DOMAIN 472 644 CYS-RICH.
FT	DOMAIN 720 987 PROTEIN KINASE.
FT	NP_BIND 726 734 ATP (BY SIMILARITY).
FT	BINDING 753 753 ATP (BY SIMILARITY).
FT	ACT_SITE 845 845 BY SIMILARITY.
PT	DISULF 195 204 BY SIMILARITY.
PT	DISULF 199 212 BY SIMILARITY.
PT	DISULF 236 244 BY SIMILARITY.
PT	DISULF 240 252 BY SIMILARITY.
PT	DISULF 255 264 BY SIMILARITY.
PT	DISULF 268 295 BY SIMILARITY.
PT	DISULF 299 311 BY SIMILARITY.
PT	DISULF 315 331 BY SIMILARITY.
PT	DISULF 334 338 BY SIMILARITY.
PT	DISULF 511 520 BY SIMILARITY.
PT	DISULF 515 528 BY SIMILARITY.
PT	DISULF 531 540 BY SIMILARITY.
PT	DISULF 544 560 BY SIMILARITY.
PT	DISULF 563 576 BY SIMILARITY.
PT	DISULF 567 584 BY SIMILARITY.
PT	DISULF 587 596 BY SIMILARITY.
PT	DISULF 600 623 BY SIMILARITY.
PT	DISULF 626 634 BY SIMILARITY.
PT	DISULF 630 642 BY SIMILARITY.
PT	MOD_RES 1139 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT MOD RES 1247 1247 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 658 658 V -> E (IN ONCOGENIC NEU).
 FT VARIANT 659 659 V -> R (IN ONCOGENIC NEU).
 SQ SEQUENCE 1254 AA; 138252 MW; 974C3791C21F2BBE1 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
 Db 1021 EBYLVPOQGF 1030

RESULT 3
 ERB2_HUMAN STANDARD; PRT; 1255 AA.
 ID ERB2_HUMAN
 AC P04626;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Receptor protein-tyrosine kinase erbB-2 precursor (BC 2.7.1.112)
 DE (p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell
 DE surface receptor HER2) (MLN 19).
 GN ERB2 OR HER2 OR NGL OR NEU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID:9606;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118663; PubMed=3003577;
 RA Yamamoto T., Ikawa S., Akiyama T., Semba K., Nomura N., Miyajima N.,
 RA Salto T., Toyoshima K.;
 RA "Similarity of protein encoded by the human c-erbB-2 gene to
 RA epidermal growth factor receptor.";
 RA Nature 319:230-234 (1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86070181; PubMed=2999974;
 RA Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,
 RA McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,
 RA Francke U., Levinson A., Ullrich A.;
 RA "Tyrosine kinase receptor with extensive homology to EGF receptor
 RA shares chromosomal location with neu oncogene.";
 RA Science 230:1132-1139 (1985).
 RN [3]
 RP SEQUENCE OF 737-1031 FROM N.A.
 RX MEDLINE=86016729; PubMed=299567;
 RA Semba K., Kamata N., Toyoshima K., Yamamoto T.;
 RA "A v-erbB-related protooncogene, c-erbB-2, is distinct from the
 RA c-erbB-1/epidermal growth factor-receptor gene and is amplified in a
 RA human salivary gland adenocarcinoma.";
 RA Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501 (1985).
 RN [4]
 RP VARIANTS VAL-654 AND VAL-655
 RX MEDLINE=93194196; PubMed=8095488;
 RA Ehsani A., Low J., Wallace R.B., Wu A.M.;
 RA "Characterization of a new allele of the human ERB2 gene by allele-
 RA specific competition hybridization.";
 RA Genomics 15:426-429 (1993).
 CC -1- FUNCTION: Essential component of a neurotrophin-receptor complex,
 CC although neurotrophins do not interact with it alone. G930 is a
 CC potential ligand for this receptor. Not activated by EGF, TGF-
 CC alpha and amphiregulin.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

CC tyrosine phosphate.
 CC -1- SUBUNIT: Heterodimer with each of the other ERB2 receptors
 CC (Potential). Interacts with PRKCAP (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
 CC residues (By similarity).
 CC -1- POLYMORPHISM: There are four alleles due to the variations in
 CC positions 654 and 655. Allele B1 (654-Ile-Ile-655) has a frequency
 CC of 0.782; allele B2 (654-Ile-Val-655) has a frequency of 0.206;
 CC allele B3 (654-Val-Val-655) has a frequency of 0.012.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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 CC -----
 CC EMBL: M1767; AAA35808.1; -;
 CC EMBL: M1761; AAA35808.1; JOINED.
 CC EMBL: M1762; AAA35808.1; JOINED.
 CC EMBL: M1763; AAA35808.1; JOINED.
 CC EMBL: M1764; AAA35808.1; JOINED.
 CC EMBL: M1765; AAA35808.1; JOINED.
 CC EMBL: M1766; AAA35808.1; JOINED.
 CC EMBL: M1730; AAA75493.1; -;
 CC EMBL: M12036; AAA35978.1; -;
 CC EMBL: X03363; CAA37060.1; -;
 CC PIR: A24571; A24571.
 CC PDB: 1N82; 18-FEB-03.
 CC PDB: 1OR1; 01-JAN-00.
 CC DR GeneW: HGNC:3430; ERB2.
 CC MIM: 164870; -;
 CC GO: GO:0005012; F:Neu/ErbB-2 receptor activity; TAS.
 CC GO: GO:0004716; F:receptor signaling protein tyrosine kinase . . . ; TAS.
 CC GO: GO:0008283; P:cell proliferation; TAS.
 CC GO: GO:0007048; P:oncogenesis; TAS.
 CC GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
 CC GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 CC InterPro: IPR000494; EGFR_L_domain.
 CC InterPro: IPR006211; Furin-like.
 CC InterPro: IPR000719; Furin repeat.
 CC InterPro: IPR000719; Prot Kinase.
 CC InterPro: IPR001245; Tyr_kinase.
 CC InterPro: IPR004019; YLP_motif.
 CC Pfam: PF00757; Furin-like; 1.
 CC Pfam: PF00069; pkinase; 1.
 CC Pfam: PF01030; Recep_L_domain; 2.
 CC Pfam: PF02757; YLP; 2.
 CC PRINTS: PRO0109; TYRKINASE.
 CC ProDom: PD000001; Prot_Kinase; 1.
 CC SMART: SM00261; FU; 4.
 CC DR SMART: SM00219; TYKC; 1.
 CC DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 CC DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC KX Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
 CC KW Transferrin; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 CC KM Polymorphism; 3D-structure.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 1255 RECEPTOR PROTEIN-TYROSINE KINASE ERB2-2.
 CC FT DOMAIN 22 652 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 653 675 POTENTIAL.
 CC FT DOMAIN 676 1255 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 720 987 PROTEIN KINASE.
 CC FT NP_BIND 726 734 ATP (BY SIMILARITY).
 CC FT BINDING 753 753 ATP (BY SIMILARITY).
 CC FT ACT_SITE 845 845 BY SIMILARITY.
 CC FT DISULFID 195 204 BY SIMILARITY.
 CC FT DISULFID 199 212 BY SIMILARITY.
 CC FT DISULFID 220 227 BY SIMILARITY.

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FT DISULFID 224 235 BY SIMILARITY.
FT DISULFID 226 244 BY SIMILARITY.
FT DISULFID 240 252 BY SIMILARITY.
FT DISULFID 255 264 BY SIMILARITY.
FT DISULFID 268 295 BY SIMILARITY.
FT DISULFID 299 311 BY SIMILARITY.
FT DISULFID 315 331 BY SIMILARITY.
FT DISULFID 334 338 BY SIMILARITY.
FT DISULFID 511 520 BY SIMILARITY.
FT DISULFID 515 528 BY SIMILARITY.
FT DISULFID 531 540 BY SIMILARITY.
FT DISULFID 544 560 BY SIMILARITY.
FT DISULFID 563 576 BY SIMILARITY.
FT DISULFID 567 584 BY SIMILARITY.
FT DISULFID 587 596 BY SIMILARITY.
FT DISULFID 600 623 BY SIMILARITY.
FT DISULFID 626 634 BY SIMILARITY.
FT DISULFID 630 642 BY SIMILARITY.
FT MOD_RES 1139 1139 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 1248 1248 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 654 654 I -> V (IN dbsnp:1801201).
FT VARIANT 655 655 I -> V (IN dbsnp:1801200).
FT VARIANT 655 655 /FtId=VAR_004078.
FT CONFLICT 1170 1170 P -> A (IN REF. 2).
FT SEQUENCE 1255 AA; 137909 MW; 359D9FDA04DC962 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 1255;
Beer Local Similarity 100.0%; Pred No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOQGF 10
Db 1021 BEYLVPOQGF 1030

RESULT 4
ERRB2 RAT STANDARD; PRT; 1257 AA.
ID _ERRB2 RAT
AC P06454;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-2 precursor (BC 2.7.1.112)
DE (p15erbB2) (NEU proto-oncogene) (C-erbB-2) (Epidermal growth factor
DE receptor-related protein).
GN ERBB2 OR NEU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Neuroblastoma;
RX MEDLINE=8611862; PubMed=3945311;
RA Bergmann C.I., Hung M.-C., Weinberg R.A.;
RT "The neu oncogene encodes an epidermal growth factor receptor-related
RT protein.";
RL Nature 319:226-230(1986).
RN [2]
RP SEQUENCE OF 852-905 FROM N.A.
RC TISSUE=Sciatic nerve;
RX MEDLINE=9122256; PubMed=2025425;
RA Lai C., Lemke G.;
RT "An extended family of protein-tyrosine kinase genes differentially
RT expressed in the vertebrate nervous system.";

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RL Neuron 6:691-704(1991).
RN [3]
RP STRUCTURE BY NMR OF 650-668.
RX MEDLINE=92155181; PubMed=1346763;
RA Guillek W.J., Bottomley A.C., Loftis F.J., Doak D.G., Mulvey D.,
RA Newman R., Crumpton M.J., Sternberg M.J.B., Campbell I.D.;
RT "Three dimensional structure of the transmembrane region of the proto-
RT oncogenic and oncogenic forms of the neu protein.";
RL EMBO J. 11:43-48(1992).
CC -I- FUNCTION: Essential component of a neurogulin-receptor complex,
CC although neurogulins do not interact with it alone. GP30 is a
CC potential ligand for this receptor. Not activated by EGF, TGF-
CC alpha, and amphiregulin.
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBUNIT: Heterodimer with each of the other ERBB receptors. The
CC constitutively activated oncogenic variant forms a homodimer.
CC Interacts with PKCABP (By similarity).
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- PTM: ligand-binding increases phosphorylation on tyrosine
CC residues (By similarity).
CC -I- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC -----
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CC -----
CC EMBL: X03362; CA27059.1; ALT_INIT.
CC PDB: 1I1J; 27-JUN-01.
CC PDB: 1N8Y; 18-FEB-03.
CC InterPro: IPR000494; EGFR_L domain.
CC InterPro: IPR006211; Furin-like.
CC InterPro: IPR006212; Furin repeat.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR001245; Tyr_kinase.
CC InterPro: IPR004019; YLP motif.
CC Pfam: PF00757; Furin-like; 1.
CC Pfam: PF00069; kinase; 1.
CC Pfam: PF01030; Recep_L_domain; 2.
CC Pfam: PF02757; YLP; 2.
CC PRINTS: PR00109; TYRKINASE.
CC PRODOM: PD000001; Prot_kinase; 1.
CC SMART: SM00261; FU; 4.
CC DR SMART; SM00219; TYRK; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
CC Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
CC Transferrase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC KW Proto-oncogene; Disease mutation; 3D-structure.
CC KX
CC FT SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 22 1257 RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
CC FT DOMAIN 22 654 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 655 677 POTENTIAL.
CC FT DOMAIN 678 1257 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 159 369 CYS-RICH.
CC FT DOMAIN 473 646 CYS-RICH.
CC FT DOMAIN 722 969 PROTEIN KINASE.
CC FT NP BIND 728 736 ATP (BY SIMILARITY).
CC FT BINDING 755 755 ATP (BY SIMILARITY).
CC FT ACT SITE 847 847 BY SIMILARITY.
CC FT DISULFID 196 205 BY SIMILARITY.
CC FT DISULFID 200 213 BY SIMILARITY.
CC FT DISULFID 221 228 BY SIMILARITY.
CC FT DISULFID 225 236 BY SIMILARITY.
CC FT DISULFID 237 245 BY SIMILARITY.
CC FT DISULFID 241 253 BY SIMILARITY.
CC FT DISULFID 256 265 BY SIMILARITY.
CC FT DISULFID 269 296 BY SIMILARITY.

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FT DISULFID 300 312 BY SIMILARITY.
FT DISULFID 316 332 BY SIMILARITY.
FT DISULFID 335 339 BY SIMILARITY.
FT DISULFID 513 522 BY SIMILARITY.
FT DISULFID 517 530 BY SIMILARITY.
FT DISULFID 533 542 BY SIMILARITY.
FT DISULFID 546 562 BY SIMILARITY.
FT DISULFID 565 578 BY SIMILARITY.
FT DISULFID 569 586 BY SIMILARITY.
FT DISULFID 589 598 BY SIMILARITY.
FT DISULFID 602 625 BY SIMILARITY.
FT DISULFID 628 636 BY SIMILARITY.
FT DISULFID 632 644 BY SIMILARITY.
FT MOD RES 1141 1141 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD RES 1250 1250 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 532 532 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 573 573 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 661 661 V -> E (IN ONCOGENIC NEU).
SO SEQUENCE 1257 AA; 138831 MW; 6129264583011402 CRC64;

Query Match 100.0%; Score 54; DB 1; Length 1257;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EHYLVPQGGF 10
Db 1023 EHYLVPQGGF 1032

RESULT 5
EGFR HUMAN STANDARD; PRT; 1210 AA.
AC P00533; O00688; O00732; P06268; Q14225; Q92795; Q9B252; Q9GZX1;
AC Q9H2C9; Q9H3C9; Q9UMD7; Q9UMD8; Q9UMG5;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112) (Receptor
protein-tyrosine kinase ErbB-1).
GN EGFR OR ERBB1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN 11
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=84219729; PubMed=6328312;
RA Ullrich A., Coussens L., Hayflick J.S., Dull T.J., Gray A., Tam A.W.,
RA Lee J., Yarden Y., Libermann T.A., Schlessinger J., Downward J.,
RA Mayer E.L.V., Whittle N., Waterfield M.D., Seeburg P.H.;
RT "Human epidermal growth factor receptor cDNA sequence and aberrant
RT expression of the amplified gene in A431 epidermoid carcinoma cells.";
RL Nature 309:418-425(1984).
RN 12
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=95382957; PubMed=7654368;
RA Ilekis J.V., Stark B.C., Scoccia B.;
RT "Possible role of variant RNA transcripts in the regulation of
RT epidermal growth factor receptor expression in human placenta.";
RL Mol. Reprod. Dev. 41:149-156(1995).
RN 13
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=97078666; PubMed=8918811;
RA Reiter J.L., Mathie N.J.;
RT "A 1.8 kb alternative transcript from the human epidermal growth
RT factor receptor gene encodes a truncated form of the receptor.";
RL Nucleic Acids Res. 24:4050-4056(1996).

RN 14
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Placenta;
RX MEDLINE=97256547; PubMed=9103388;
RA Ilekis J.V., Garfili J., Niederberger C., Scoccia B.;
RT "Expression of a truncated epidermal growth factor receptor-like
RT protein (TEGFR) in ovarian cancer.";
RL Gynecol. Oncol. 65:36-41(1997).
RN 15
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RC TISSUE=Placenta;
RX MEDLINE=21100872; PubMed=11161793;
RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielsen A.J.,
RA Scheel Sinclair C., Pearall R.S., Green P.J., Yee D., Lampfand A.L.,
RA Balasubramaniam S., Crossley T.D., Magnuson T.R., James C.D.,
RA Mathie N.J.;
RT "Comparative genomic sequence analysis and isolation of human and
RT mouse alternative EGFR transcripts encoding truncated receptor
RT isoforms.";
RL Genomics 71:1-20(2001).
RN 16
RP SEQUENCE OF 575-687 FROM N.A.
RA Reiter J.L., Threadgill D.W., Danielsen A.J., Scheel C.M.,
RA Lampfand A.L., Balasubramaniam S., Crossley T.O., Magnuson T.R.,
RA Mathie N.J.;
RT "Human and mouse alternative EGFR transcripts encoding only the
RT extracellular domain of the receptor.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN 17
RP SEQUENCE OF 713-924 FROM N.A.
RX MEDLINE=84196372; PubMed=6326261;
RA Lin C.R., Chen W.S., Kruliger W., Stolarsky L.S., Weber W.,
RA Evans R.M., Verma I.M., Gill G.N., Rosenfeld M.G.;
RT "Expression cloning of human EGF receptor complementary DNA: Gene
RT amplification and three related messenger RNA products in A431
RT cells.";
RL Science 224:843-848(1984).
RN 18
RP SEQUENCE OF 150-962 FROM N.A.
RX MEDLINE=84245835; PubMed=6330563;
RA Xu Y.H., Ishii S., Clark A.J.L., Sullivan M., Wilson R.K., Ma D.P.,
RA Roe B.A., Merlino G.T., Pastan I.;
RT "Human epidermal growth factor receptor cDNA is homologous to a
RT variety of RNAs overproduced in A431 carcinoma cells.";
RL Nature 309:806-810(1984).
RN 19
RP SEQUENCE OF 1028-1210 FROM N.A.
RX MEDLINE=85046483; PubMed=6093780;
RA Simmen F.A., Gope M.L., Schulz T.Z., Wright D.A., Carpenter G.,
RA O'Malley B.W.;
RT "Isolation of an evolutionarily conserved epidermal growth factor
RT receptor cDNA from human A431 carcinoma cells.";
RL Biochem. Biophys. Res. Commun. 124:125-132(1984).
RN 10
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=88217333; PubMed=3329716;
RA Haley J.D., Whittle N., Bennett P., Kinchington D., Ullrich A.,
RA Waterfield M.D.;
RT "The human EGF receptor gene: structure of the 110 kb locus and
RT identification of sequences regulating its transcription.";
RL Oncogene Res. 1:375-396(1987).
RN 11
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=91107677; PubMed=1988448;
RA Haley J.D., Waterfield M.D.;
RT "Contributory effects of de novo transcription and premature
RT transcript termination in the regulation of human epidermal growth
RT factor receptor proto-oncogene RNA synthesis.";
RL J. Biol. Chem. 266:1746-1753(1991).
RN 12
RP SEQUENCE OF 1-29 FROM N.A.
RX MEDLINE=85270438; PubMed=2991899;
RA Ishii S., Xu Y.H., Stratton R.H., Roe B.A., Merlino G.T., Pastan I.;
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RT "Characterization and sequence of the promoter region of the human
RT epidermal growth factor receptor gene.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:4920-4924 (1985).
RN [13]
RP SEQUENCE OF 540.
RA Kohda D.;
RA Submitted (SEP-1997) to the SWISS-PROT data bank.
RN [14]
RP RECEPTOR ACTIVITY.
RX MEDLINE=84191554; PubMed=6325948;
RA "Mroczkowski B., Mosig G., Cohen S.;
RT "ATP-stimulated interaction between epidermal growth factor receptor
RT and supercoiled DNA.";
RL Nature 309:270-273 (1984).
RN [15]
RP PHOSPHORYLATION.
RX MEDLINE=89278137; PubMed=2543678;
RA Margolis B.L., Lax I., Kris R., Dombalagian M., Honegger A.M.,
RA Howk R., Givol D., Ullrich A., Schlessinger J.;
RT "All autophosphorylation sites of epidermal growth factor (EGF)
RT receptor and HER2/neu are located in their carboxyl-terminal tails.
RT Identification of a novel site in EGF receptor.";
RL J. Biol. Chem. 264:10667-10671 (1989).
RN [16]
RP CARBOHYDRATE-LINKAGE SITES ASN-128; ASN-175; ASN-413; ASN-444 AND
RP ASN-528.
RX MEDLINE=96398132; PubMed=8962717;
RA Smith K.D., Davies M.J., Bailey D., Renouf D.V., Hounsell E.F.;
RT "Analysis of the glycosylation patterns of the extracellular domain of
RT the epidermal growth factor receptor expressed in Chinese hamster
RT ovary fibroblasts.";
RL Growth Factors 13:121-132 (1996).
RN [17]
RP CARBOHYDRATE-LINKAGE SITES ASN-56; ASN-352; ASN-361; ASN-568 AND
RP ASN-603.
RX MEDLINE=20198209; PubMed=10731668;
RA Sato C., Kim J.-H., Abe Y., Saito K., Yokoyama S., Kohda D.;
RT "Characterization of the N-Oligosaccharides attached to the atypical
RT Asn-X-Cys sequence of recombinant human epidermal growth factor
RT receptor.";
RL J. Biochem. 127:65-72 (2000).
RN [18]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=98225196; PubMed=9556602;
RA Abe Y., Ooka M., Inagaki F., Lax I., Schlessinger J., Kohda D.;
RT "Disulfide bond structure of human epidermal growth factor receptor.";
RL J. Biol. Chem. 273:11150-11157 (1998).
RN [19]
RP REVIEW.
RX MEDLINE=87297456; PubMed=3039909;
RA Carpenter G.;
RT "Receptors for epidermal growth factor and other polypeptide
RT mitogens.";
RL Annu. Rev. Biochem. 56:881-914 (1987).
RN [20]
RP INTERACTION WITH RPKL.
RX PubMed=1116146;
RA Habbib A.A., Chatterjee S., Park S.-K., Ratan R.R., Lefebvre S.,
RA Vartanian T.;
RT "The epidermal growth factor receptor engages receptor interacting
RT protein and nuclear factor-kappa B (NF-kappa B)-inducing kinase to
RT activate NF-kappa B. Identification of a novel receptor-tyrosine
RT kinase signalosome.";
RL J. Biol. Chem. 276:8865-8874 (2001).
RN [21]
RP FUNCTION: Receptor for EGF, but also for other members of the EGF
CC family, as TGF-alpha, amphiregulin, betacellulin, heparin-binding
CC EGF-like growth factor, gp30 and vaccinia virus growth factor. Is
CC involved in the control of cell growth and differentiation.
CC -1- FUNCTION: Isoform 2/truncated isoform may act as an antagonist.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: Binds RPKL.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is

CC secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1; Synonyms=pl10;
CC Name=2; Synonyms=pl11; Sequence=Displayed;
CC Name=3; Synonyms=pl12; Sequence=VSP_002887; VSP_002888;
CC Name=4; Synonyms=pl13; Sequence=VSP_002889; VSP_002890;
CC Name=5; Synonyms=pl14; Sequence=VSP_002891; VSP_002892;
CC -1- TISSUE SPECIFICITY: Expressed in placenta. Isoform 2 is also
CC expressed in ovarian cancers.
CC -1- MISCELLANEOUS: Binding of EGF to the receptor leads to
CC dimerization, internalization of the EGF-receptor complex,
CC induction of the tyrosine kinase activity, stimulation of cell DNA
CC
Query Match 92.6%; Score 50; DB 1; Length 1210;
Best Local Similarity 80.0%; Pred. No. 0.066;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
DB 1014 DEVLIP00GF 1023
QY 1 DEVLIP00GF 10
ID EGRF_MOUSE STANDARD; PRT; 1210 AA.
AC 001279;
DT 01-FEB-1996 (Rel. 33; Created)
DT 01-FEB-1996 (Rel. 33; Last sequence update)
DT 15-SEP-2003 (Rel. 42; Last annotation update)
DE Epidermal growth factor receptor precursor (EC 2.7.1.112).
GN EGRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=93026370; PubMed=1408137;
RA Avitv A., Skorecki K., Yayon A., Givol D.;
RT "Promoter region of the murine fibroblast growth factor receptor 2
RT (bek/KGFR) gene.";
RL Oncogene 7:1957-1962 (1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c, and CD-1; TISSUE=Decidua, and Liver;
RX MEDLINE=93126380; PubMed=7678348;
RA Paria B.C., Das S.K., Andrews G.K., Day S.K.;
RT "Expression of the epidermal growth factor receptor gene is regulated
RT in mouse blastocysts during delayed implantation.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:55-59 (1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Hibbs M.L.;
RT Submitted (APR-1994) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=B6/C3; TISSUE=Liver;
RX MEDLINE=94170986; PubMed=8125255;
RA Luetteke N.C., Phillips H.K., Qiu T.H., Copeland N.G., Eard H.S.,
RA Jenkins N.A., Lee D.C.;
RT "The mouse waved-2 phenotype results from a point mutation in the EGF
RT receptor tyrosine kinase.";
RL Gene Dev. 8:399-413 (1994).
RN [5]
RP SEQUENCE OF 1-714 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91232866; PubMed=2030916;

RA Avila A., Lax I., Ullrich A., Schlessinger J., Givol D., Morse B.;
 RT "Comparison of EGF receptor sequences as a guide to study the ligand
 RT binding site.";
 RL Oncogene 6:673-676(1991).
 RN [6]
 RP SEQUENCE OF 969-1117 FROM N.A.
 RC STRAIN-C3H;
 RA Bisinger D.P., Serrero G.;
 RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE EGF RECEPTOR MEDIATES THE BIOLOGICAL SIGNAL OF EGF.
 CC AND ALSO OF TGF-ALPHA, AMPHIREGULIN, HEPARIN-BINDING EGF, GP30 AND
 CC VACCINIA VIRUS GROWTH FACTOR (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Binds RIRK1 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- MISCELLANEOUS: Binding of EGF to the receptor leads to
 CC dimerization, internalization of the EGF-receptor complex,
 CC induction of the tyrosine kinase activity, stimulation of cell DNA
 CC synthesis, and cell proliferation.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X78987; CAAS5587.1; -;
 CC EMBL; U03425; AAA1789.1; -;
 CC EMBL; X59698; CAA4219.1; -;
 CC EMBL; L06864; AAA53029.1; -;
 CC EMBL; Z12608; CAA78249.1; -;
 CC FIR; A53183; A53183.
 CC HSSP; P11362; 1FGK.
 CC MGD; MGI:95294; Egfr.
 CC GO; GO:0005622; C:intracellular; IDA.
 CC GO; GO:0005622; C:intracellular; IDA.
 CC InterPro; IPR000494; EGFR_L_domain.
 CC InterPro; IPR006211; Furin-like.
 CC InterPro; IPR006212; Furin repeat.
 CC InterPro; IPR000719; Prot_kinase.
 CC InterPro; IPR001245; Tyr_kinase.
 CC Pfam; PF000757; Furin-like; 1.
 CC Pfam; PF000659; Kinase; 1.
 CC Pfam; PF01030; Recep_L_domain; 2.
 CC PRINTS; PR00109; TYRKINASE.
 CC ProDom; PD000001; Prot_kinase; 1.
 CC SMART; SM00219; TyrKc; 1.
 CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 CC Transmembrane; Glycoprotein; Receptor; Signal; Transferase;
 CC Tyrosine-protein kinase; ATP-binding; Phosphorylation; Repeat.
 CC SIGNAL 1 24
 CC CHAIN 25 1210
 CC DOMAIN 25 647
 CC TRANSMEM 648 670
 CC DOMAIN 671 1210
 CC REPEAT 75 300
 CC REPEAT 390 600
 CC DOMAIN 1028 1071
 CC DOMAIN 714 981
 CC NP_BIND 720 728
 CC BINDING 747 747
 CC ACT_SITE 839 839
 CC DISULFID 190 199
 CC DISULFID 194 207
 CC DISULFID 215 223
 CC DISULFID 219 231
 CC BY SIMILARITY.

FT DISULFID 232 240 BY SIMILARITY.
 FT DISULFID 236 248 BY SIMILARITY.
 FT DISULFID 251 260 BY SIMILARITY.
 FT DISULFID 264 291 BY SIMILARITY.
 FT DISULFID 295 307 BY SIMILARITY.
 FT DISULFID 311 326 BY SIMILARITY.
 FT DISULFID 329 333 BY SIMILARITY.
 FT DISULFID 506 515 BY SIMILARITY.
 FT DISULFID 510 523 BY SIMILARITY.
 FT DISULFID 526 535 BY SIMILARITY.
 FT DISULFID 539 555 BY SIMILARITY.
 FT DISULFID 558 571 BY SIMILARITY.
 FT DISULFID 562 579 BY SIMILARITY.
 FT DISULFID 582 591 BY SIMILARITY.
 FT DISULFID 595 617 BY SIMILARITY.
 FT DISULFID 620 628 BY SIMILARITY.
 FT DISULFID 624 636 BY SIMILARITY.
 FT MOD_RES 680 680
 FT MOD_RES 1092 1092
 FT MOD_RES 1110 1110
 FT MOD_RES 1172 1172
 FT MOD_RES 1197 1197
 FT CARBOHYD 128 128
 FT CARBOHYD 175 175
 FT CARBOHYD 196 196
 FT CARBOHYD 352 352
 FT CARBOHYD 413 413
 FT CARBOHYD 444 444
 FT CARBOHYD 528 528
 FT CARBOHYD 568 568
 FT CARBOHYD 603 603
 FT CARBOHYD 623 623
 FT CONFLICT 19 19
 FT CONFLICT 539 539
 FT CONFLICT 991 991
 FT CONFLICT 1117 1117
 SQ SEQUENCE 1210 AA; 134853 MW; 690E20D46D2F5 CRC64;
 Query Match: 92.6%; Score 50; DB 1; Length 1210;
 Best Local Similarity 80.0%; Pred. No. 0.066; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 0;
 Qy 1 EBYLVPQGGF 10
 Db 1016 DEYLIPQGGF 1025
 RESULT 7
 ERBB_AVIEU STANDARD; PRT; 540 AA.
 ID ERBB_AVIEU
 AC P11273;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 GN Tyrosine-protein kinase transforming protein erbB (BC 2.7.1.112).
 GN v-ERBB.
 OS Avian erythroblastosis virus (strain ts167).
 OC Viruses; Retroviral viruses; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxID=103898;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87064458; PubMed=2878364;
 RA Choi O.R., Trainor C., Graf T., Beug H., Engel J.D.;
 RT "A single amino acid substitution in v-erbB confers a thermolabile
 RT phenotype" to ts167 avian erythroblastosis virus-transformed erythroid
 RT cells.";
 RL Mol. Cell. Biol. 6:1751-1759(1986).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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CC -----
 DR EMBL; M13179; AAA42401.1; -
 DR PIR; A25231; TVFVEB.
 DR HSSP; P1362; 1FGK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinae; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Oncogene;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 132 399
 FT NP BIND 138 146 ATP (BY SIMILARITY).
 FT BINDING 165 165 ATP (BY SIMILARITY).
 FT ACT_SITE 257 257 BY SIMILARITY.
 FT ACT_SITE 257 257 H -> D (IN THERMOLABILE V-ERBB).
 FT VARIANT 270 270
 SQ SEQUENCE 540 AA; 60412 MW; 5B53297AA068B65D CRC64;

Query Match 85.2%; Score 46; DB 1; Length 540;
 Best Local Similarity 80.0%; Pred. No. 0.19;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
 Db 434 DEYLVPHQGF 443

RESULT 8
 ERBB AVIER STANDARD; PRT; 604 AA.
 ID ERBB AVIER
 AC P00535;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
 GN V-ERBB.
 OS Avian erythroblastosis virus (strain BS4).
 OC Viruses; Retrovirdae; Retroviridae; Avian type C retroviruses.
 OX NCBI_TaxId=79685;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=H;
 RX MEDLINE=84026539; PubMed=633222;
 RA Yamamoto T., Nishida T., Miyajima N., Kawai S., Ooi T., Toyoshima K.;
 RT "The erbB gene of avian erythroblastosis virus is a member of the src
 RT gene family.";
 RL Cell 35:71-78(1983).

RT [2]
 RP SEQUENCE OF 1-152 FROM N.A.
 RX MEDLINE=84223957; PubMed=6328658;
 RA Debilitre B., Henry C., Benaisa M., Biserle G., Claverie J.-M.,
 RA Sauls S., Martin P., Stehelin D.;
 RT "Sequencing the erbA gene of avian erythroblastosis virus reveals a
 RT new type of oncogene.";
 RL Science 224:1456-1459(1984).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- DISEASE: THE V-ERBB ONCOGENE TRANSFORMS AVIAN FIBROBLASTS AND
 CC ERYTHROBLASTS IN CULTURE AND INDUCES SARCOMA AND ERYTHROLEUKEMIAS
 CC IN CHICKENS.
 CC -1- MISCELLANEOUS: V-ERBB IS A TRUNCATED AND MUTATED VERSION OF THE
 CC RECEPTOR FOR EPIDERMAL GROWTH FACTOR.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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CC -----
 DR EMBL; K02006; AAA42394.1; ALT_INIT.
 DR EMBL; K01216; AAA42400.1; -
 DR PIR; A00644; TVYH.
 DR HSSP; P1362; 1FGK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; pkinae; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SMO0219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase; Tyrosine-protein kinase; ATP-binding; Oncogene;
 KW Glycoprotein; Phosphorylation.
 FT DOMAIN 132 399
 FT NP BIND 138 146 ATP (BY SIMILARITY).
 FT BINDING 165 165 ATP (BY SIMILARITY).
 FT ACT_SITE 257 257 BY SIMILARITY.
 FT ACT_SITE 257 257 R -> W (IN REF. 2).
 FT CONFLICT 140 140 S -> F (IN REF. 2).
 FT CONFLICT 146 146 I -> V (IN REF. 2).
 SQ SEQUENCE 604 AA; 67633 MW; 76B8CD06745D609 CRC64;

Query Match 85.2%; Score 46; DB 1; Length 604;
 Best Local Similarity 80.0%; Pred. No. 0.21;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
 Db 434 DEYLVPHQGF 443

RESULT 9
 ERBB ALV STANDARD; PRT; 634 AA.
 ID ERBB ALV
 AC P00534;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase transforming protein erbB (EC 2.7.1.112).
 GN V-ERBB.
 OS Avian leukosis virus.
 OC Viruses; Retrovirdae; Retroviridae; Alpharetrovirus.
 OX NCBI_TaxId=11864;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85228222; PubMed=2988784;
 RA Nielsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
 RA Crittenden L.B., Raines M.A., Kung H.-J.;
 RT "c-erbB activation in ALV-induced erythroblastosis: novel RNA
 RT processing and promoter insertion result in expression of an
 RT amino-truncated EGF receptor.";
 RL Cell 41:719-726(1985).

RT [2]
 RP SEQUENCE OF 1-152 FROM N.A.
 RX MEDLINE=85228222; PubMed=2988784;
 RA Nielsen T.W., Maroney P.A., Goodwin R.G., Rottman F.M.,
 RA Crittenden L.B., Raines M.A., Kung H.-J.;
 RT "c-erbB activation in ALV-induced erythroblastosis: novel RNA
 RT processing and promoter insertion result in expression of an
 RT amino-truncated EGF receptor.";
 RL Cell 41:719-726(1985).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS PRODUCED BY ERYTHROLEUKEMIA CELLS
 CC IN CHICKS WHICH HAVE BEEN INJECTED WITH THE AVIAN LEUKOSIS VIRUS
 CC AND SUBSEQUENTLY DEVELOP LEUKEMIA. THE LEUKEMIAS ARE INDUCED BY
 CC THE INSERTION OF RETROVIRAL PROMOTER ELEMENTS IN OR NEAR THE
 CC C-ERBB GENE, WHICH LEADS TO C-ERBB ACTIVATION.
 CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED AS A GAG-ENV-ERBB
 CC PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.

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DR EMBL; M10066; AAA48763.1; ALT_INIT.
DR HSSP; P11362; IFGK.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR TRANSFERASE; Tyrosine-protein kinase; ATP-binding; Oncogene;
KW Glycoprotein; Phosphorylation.
FT DOMAIN 132 399 PROTEIN_KINASE.
FT NP_BIND 138 146 ATP (BY SIMILARITY).
FT BINDING 165 165 ATP (BY SIMILARITY).
FT ACT_SITE 257 257 BY SIMILARITY.
SQ SEQUENCE 634 AA; 70891 MW; E705E33A0BE01FCC CRC64;

Query Match 85.2%; Score 46; DB 1; Length 634;
Best Local Similarity 80.0%; Pred. No. 0.22;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EBYLVPQGGF 10
Db 434 DEYLPHQGF 443

RESULT 10
YH73 SYNY3 STANDARD; PRT; 232 AA.
AC P73623;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein a111773.
GN SL11773.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
ON NCB1_TaxID=1148;
RX MEDLINE=97061201; Pubmed=8905231;
RA Kaneo T., Sato S., Kocani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugitani M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
RA Shimoto S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions";
RL DNA Res. 3:109-136(1996).
CC -1- SIMILARITY: BELONGS TO THE PIRIN FAMILY.
CC -----
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DR EMBL; D90908; BAA17668.1; -.
DR PIR; S77110; S77110.

DR InterPro; IPR007113; Cupin_sup.
DR InterPro; IPR003829; DUF209.
DR Pfam; PF02678; Pirin; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 232 AA; 25700 MW; 09B9DCC5352AA70 CRC64;

Query Match 70.4%; Score 38; DB 1; Length 232;
Best Local Similarity 60.0%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EBYLVPQGGF 10
Db 45 EDYIAPQGGF 54

RESULT 11
ERB4_MOUSE
ID ERB4_MOUSE STANDARD; PRT; 95 AA.
AC Q61527;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Receptor protein-tyrosine kinase erbB-4 (BC 2.7.1.112) (Fragments).
GN ERB4 OR HER4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCB1_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-27 FROM N.A. (ISOFORMS JM-A AND JM-B).
RC TISSUE=Heart, and Kidney;
RX MEDLINE=97476287; Pubmed=9334263;
RA Elenius K., Corfas G., Paul S., Choi C.J., Rito C., Plozman G.D.,
RA Klasebrun M.;
RT "A novel juxtamembrane domain isoform of HER4/ErbB4. Isoform-specific
RT tissue distribution and differential processing in response to
RT phorbol ester";
RL J. Biol. Chem. 272:26761-26768(1997).
RN [2]
RP SEQUENCE OF 28-95 FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=96069911; Pubmed=7589796;
RA Nicosco L.M., Chu G.C., Gautam M., Noakes P.G., Merlie J.P.,
RA Sanes J.R.;
RT "Synapse-associated expression of an acetylcholine receptor-inducing
RT protein, ARIA/hergulin, and its putative receptors, ErbB2 and ErbB3,
RT in developing mammalian muscle";
RL Dev. Biol. 172:158-169(1995).
CC -1- FUNCTION: Specifically binds and is activated by neuregulin, NRG-
CC 2, NRG-3, heparin-binding EGF-like growth factor, betacellulin and
CC NTAK. Interaction with these factors induces cell differentiation.
CC Not activated by BGF, TGF-A, and amphiregulin (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphatase.
CC -1- SUBUNIT: Homodimer or heterodimer with each of the other ERBB
CC receptors. Interacts with the PDZ domain of the synaptrophin SNTB2
CC (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=The 2 isoforms differ functionally in their response to
CC phorbol ester: isoform JM-A is processed but not isoform JM-B.
CC So, they respectively represent cleavable and noncleavable
CC forms of the receptor. Both isoforms are expressed in
CC cerebellum, cerebral cortex, spinal cord, medulla oblongata,
CC and eye, but the kidney expresses solely isoform JM-A and the
CC heart solely isoform JM-B;
CC Name=JM-A;
CC IsoId=Q61527-1; Sequence=Displayed;
CC Name=JM-B;
CC IsoId=Q61527-2; Sequence=VSP_002896;
CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
CC residues.

```
CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
CC -----
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CC -----
CC EMBL: L47241; AAA93534.1;
CC MGD; MGJ:104771; ErbB4.
CC GO; GO:0045165; P:cell fate commitment; IDA.
CC GO; GO:0007507; P:heart development; IMP.
CC GO; GO:0007399; P:neurogenesis; IMP.
CC InterPro: IPR000719; Prot Kinase.
CC InterPro: IPR001245; Tyr Kinase.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; PARTIAL.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; PARTIAL.
CC Transmembrane; Glycoprotein; Multigene family; Receptor; Transferase;
CC Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC Alternative splicing.
CC FT NON_TER 1
CC FT NON_CONS 27 28 NGPTSHDCIYYPWTGSHLPQHA -> IGSSIEDICIGLTD
CC FT VARSPLIC 3 (in isoform JM-B).
CC FT /FTID=VSP_002896.
CC FT NON_TER 95 95
CC FT SEQUENCE 95 AA; 10524 MW; B43D0E99591744D8 CRC64;
SQ
Query Match
Best Local Similarity 100.0%; Score 37; DB 1; Length 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EBYLVPQ 7
DB 29 EBYLVPQ 35
RESULT 12
TGM2 BOVIN STANDARD; PRT; 687 AA.
AC P51176;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) (Tissue
DE transglutaminase) (TCase C) (TGC) (TG(C)) (Transglutaminase 2).
GN TGM2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
OX [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 79-95; 157-166; 242-251 AND
RP 581-587.
RC TISSUE=artery;
RX MEDLINE=92037637; PubMed=1682150;
RA Nakamishi K., Nara K., Hagiwara H., Aoyama Y., Ueno H., Hirose S.;
RT "Cloning and sequence analysis of cDNA clones for bovine aortic-
RT endothelial-cell transglutaminase.";
RL Eur. J. Biochem. 202:15-21(1991).
CC -1- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
CC CONJUGATION OF POLYAMINES TO PROTEINS.
CC -1- CATALYTIC ACTIVITY: Protein glutamine + alkylamine = protein N(5)-
CC alkylglutamine + NH(3).
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS ARE DETECTED IN THE LUNG. LOWER
CC LEVELS ARE FOUND IN THE LIVER, SPLEEN AND HEART, BUT NOT IN THE
CC BRAIN.
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CC -1- INDUCTION: By retinoic acid.
CC -----
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CC -----
CC EMBL: X60866; CAA43097.1;
CC PIR; S19680; S19680.
CC HSP; P00488; IQRK.
CC InterPro: IPR001102; Glutransfg.
CC InterPro: IPR002931; Transglutaminase-like.
CC pfam; PF01841; Transglut_core; 1.
CC pfam; PF00927; Transglutamin_C; 2.
CC pfam; PF00868; Transglutamin_N; 1.
CC SMART; SM00460; TGC; 1.
CC PROSITE; PS00547; TRANSGLUTAMINASES; 1.
CC Transferase; Acyltransferase; Calcium-binding.
CC ACT_SITE 277 BY SIMILARITY.
CC ACT_SITE 335 BY SIMILARITY.
CC ACT_SITE 335 BY SIMILARITY.
CC ACT_SITE 358 BY SIMILARITY.
CC METAL 398 CALCIUM (BY SIMILARITY).
CC METAL 400 CALCIUM (BY SIMILARITY).
CC METAL 447 CALCIUM (BY SIMILARITY).
CC METAL 452 CALCIUM (BY SIMILARITY).
CC SEQUENCE 687 AA; 77112 MW; 7BBA00F15E779944 CRC64;
SQ
Query Match
Best Local Similarity 60.0%; Score 37; DB 1; Length 687;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EBYLVPQ 10
DB 157 QEYVLTPQGF 166
RESULT 13
TGM2 HUMAN STANDARD; PRT; 687 AA.
AC P21980; Q16436; Q9BTWY; Q9UH35;
DT 01-AUG-1991 (Rel. 19, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) (Tissue
DE transglutaminase) (TCase C) (TGC) (TG(C)) (Transglutaminase 2)
DE (TCase-H).
GN TGM2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND PARTIAL SEQUENCE.
RP TISSUE=Endothelial cells;
RX MEDLINE=91093168; PubMed=1670766;
RA Gentile V., Saydak M., Chiozza B.A., Akande O., Birkbichler P.J.,
RA Lee K.N., Stein J.P., Davies P.J.A.;
RT "Isolation and characterization of cDNA clones to mouse macrophage
RT and human endothelial cell tissue transglutaminases.";
RL J. Biol. Chem. 266:478-483(1991).
CC [2]
CC SEQUENCE FROM N.A. (ISOFORM 2).
CC MEDLINE=93054562; PubMed=1358880;
CC Fraj B.M., Birkbichler P.J., Patterson M.K. Jr., Lee K.N.,
CC Gonzales R.A.;
CC "A retinoic acid-inducible mRNA from human erythroleukemia cells
CC encodes a novel tissue transglutaminase homologue.";
CC J. Biol. Chem. 267:22616-22623(1992).
CC [3]
```

RP SEQUENCE FROM N.A. (ISOFORM 3)
RX MEDLINE=96201707; PubMed=8611626;
RA Freif J.B.M., Gonzales R.A.,
RT "A third human tissue transglutaminase homologue as a result of
alternative gene transcripts."
RL Blochim. Biophys. Acta 1306:53-74(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX MEDLINE=21638749; PubMed=11780052;
RA Delonias P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Jones M., Stevirides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A.G., Coville G.J., Deedman R., Dhanraj P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahm D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath F.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levesaile M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McComachie L.J., Mclay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Pratchallang S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Showkhen R., Sims S.,
RA Skuce C.D., Smith M.L., Sodegund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitcaker P., Willey D.L., Williams R., Bentley D.R., Beck S.,
RA Wilming L., Wray P.W., Hubbard T., Duthin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX TISSUE=Kidney;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang X., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,
RA Stetson M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Tohyuk S., Carninci P., Pange C.,
RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McBean P.J., McKernan K.J., Malek U.A., Gnatrante P.H.,
RA Richards S., Wotley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodegund E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Roderieffed Y.S.N., Kirzyanski M.I., Skalska S., Smalls D.E.,
RA Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [1]
RP FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
CC CONJUGATION OF POLYAMINES TO PROTEINS.
CC -1- CATALYTIC ACTIVITY: Protein glutamine + alkylamine = protein N(5)
CC alkylglutamine + NH(3).
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Monomer.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC Isoacid=P21980-1; Sequence=Displayed;
CC Name=2;
CC Isoacid=P21980-2; Sequence=VSP_006411, VSP_006412;
CC Name=3; Synonyms=TGH2;

```

CC      -1- INDUCTION: By retinoic acid.
CC      -1- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
CC
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CC      or send an email to license@isb-sib.ch).
CC
DR      EMBL; M55153; AAA63361.1; -
DR      EMBL; M96478; AAA63739.1; -
DR      EMBL; S81734; AAB36379.1; -
DR      EMBL; AL031651; CAB66115.1; -
DR      EMBL; AL031651; CAB66116.1; -
DR      EMBL; BC003551; AAB03551.1; -
DR      PIR; A39045; A39045.
DR      PIR; S68092; S68092.
DR      PDB; 1FAU; 21-JUL-00.
DR      PDB; 1KV3; 13-MAR-02.
DR      Genew; HGNC:11778; TGM2.
DR      MIM; 190196; -.
DR      GO; GO:0006464; P:protein modification; TAS.
DR      InterPro; IPR001102; Glutaminase.
DR      InterPro; IPR002931; Transglutaminase.
DR      Pfam; PF01841; Transglut_core; 1.
DR      Pfam; PF00927; Transglutamin_C; 2.
DR      Pfam; PF00868; Transglutamin_N; 1.
DR      SMART; SMO0460; TGC; 1.
DR      PROSITE; PS00547; TRANSGLUTAMINASES; 1.
DR      Trnstraease; Acyltransferase; Calcium-binding; Alternative splicing;
KW      3D-structure.
FT      ACT_SITE 277 277
FT      ACT_SITE 335 335
FT      ACT_SITE 358 358
FT      ACT_SITE 398 398
FT      METAL 400 400
FT      METAL 447 447
FT      METAL 452 452
FT      VASPLIC 539 548
FT      VASPLIC 549 687
FT      VASPLIC 287 349
FT      VASPLIC 350 687
FT      CONFLICT 51 51
FT      CONFLICT 186 186
FT      CONFLICT 224 224
FT      CONFLICT 533 533
FT      CONFLICT 655 655
SQ      SEQUENCE 687 AA; 77328 MW; 7DA33F335DE7B37 CRC64;
Query Match 68.5%; Score 37; DB 1; Length 687;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 EBYLVPOOGF 10
DB 157 QBYLVTOOGF 166
RESULT 14
TGM2_CAVCU STANDARD; PRT; 669 AA.
ID TGM2_CAVCU
AC P08587;
DT 01-AUG-1998 (Rel. 08, Created)

```

DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) (Tissue
 DE transglutaminase) (Tgase C) (TGC) (TGC(C)) (Transglutaminase 2).
 GN TGM2.
 OS Cavia cutleri (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
 OX NCBI_TaxId=10144;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88294033; PubMed=2900023;
 RA Ikura K., Nasu T.-A., Yokota H., Teuchiya Y., Sasaki R., Chiba H.;
 RT "Amino acid sequence of guinea pig liver transglutaminase from its
 RT cDNA sequence.";
 RL Biochemistry 27:2898-2905(1988).
 RN [2]
 RP SEQUENCE OF 188-631 FROM N.A.
 RC TISSUE=Liver;
 RA Ikura K., Nasu T.-A., Yokota H., Sasaki R., Chiba H.;
 RT "Cloning of cDNA coding for guinea pig liver transglutaminase.";
 RL Agric. Biol. Chem. 51:957-961(1987).
 RN [3]
 RP SEQUENCE OF 1-4.
 RC TISSUE=Liver;
 RX MEDLINE=7111445; PubMed=5543674;
 RA Connellan J.M., Chung S.I., Wetzzel N.K., Bradley L.M., Folk J.E.;
 RT "Structural properties of guinea pig liver transglutaminase.";
 RL J. Biol. Chem. 246:1093-1098(1971).
 CC -1- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE
 CC CONJUGATION OF POLYAMINES TO PROTEINS.
 CC -1- CATALYTIC ACTIVITY: Protein glutamine + alkylamine = protein N(5)-
 CC alkylglutamine + NH(3).
 CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SIMILARITY: BELONGS TO THE TRANSGLUTAMINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; M16646; AAA37056.1; -;
 DR EMBL; D00114; BAA00068.1; -;
 DR HSSP; P00488; ICGU.
 DR InterPro: IPR001102; Glutransfg.
 DR InterPro: IPR002931; Transglutaminase-like.
 DR Pfam: PF01861; Transgluc_core; 1.
 DR Pfam: PF00927; Transglutamin_C; 2.
 DR Pfam: PF00868; Transglutamin_N; 1.
 DR SMART; SMO0460; TGC; 1.
 DR PROSITE; PS00547; TRANSGLUTAMINASES; 1.
 DR Transference; Acyltransferase; Calcium-binding.
 FT INIT MET 0
 FT MOD_RES 1
 FT ACT_SITE 276
 FT ACT_SITE 334
 FT ACT_SITE 357
 FT METAL 397
 FT METAL 399
 FT METAL 445
 FT METAL 450
 FT CONFLICT 1
 FT CONFLICT 291
 FT CONFLICT 335
 FT SEQUENCE 689 AA; 77010 MW; 05E8A2794340DAF8 CRC64;
 Query Match 68.5%; Score 37; DB 1; Length 689;

Best local similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ERYLPOQGF 10
 DB 156 QERYLPOQGF 165
 RESULT 15
 ERYB4_HUMAN STANDARD; PRT; 1308 AA.
 ID ERYB4_HUMAN
 AC Q15303;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Receptor protein-tyrosine kinase erbB-4 precursor (EC 2.7.1.112)
 DE (p180erbB4) (Tyrosine kinase-type cell surface receptor HER4).
 GN ERBB4 OR HER4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM JM-A).
 RC TISSUE=Breast carcinoma;
 RX MEDLINE=93189574; PubMed=8383326;
 RA Plozman G.D., Culoscou J.-M., Whitney G.S., Green J.M., Carlton G.W.,
 RA Foy L., Neubauer M.G., Shoyab M.;
 RT "Ligand-specific activation of HER4/p180erbB4, a fourth member of the
 RT epidermal growth factor receptor family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:1746-1750(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS JM-A AND JM-B).
 RC TISSUE=Fetal brain;
 RX MEDLINE=97476287; PubMed=9334263;
 RA Elenius K., Cortes G., Paul S., Choi C.J., Rio C., Plozman G.D.,
 RA Klagesbrunn M.;
 RT "A novel juxtamembrane domain isoform of HER4/Erbb4. Isoform-specific
 RT tissue distribution and differential processing in response to
 RT phorbol ester.";
 RL J. Biol. Chem. 272:26761-26768(1997).
 RN [3]
 RP INTERACTION WITH SNTB2.
 RX MEDLINE=20202681; PubMed=10725395;
 RA Garcia R.A., Vasudevan K., Buonanno A.;
 RT "The neurotrophin receptor ErbB-4 interacts with PDZ-containing proteins
 RT at neuronal synapses.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:3596-3601(2000).
 CC -1- FUNCTION: Specifically binds and is activated by neurotrophins, NRG-
 CC 2, NRG-3, heparin-binding EGF-like growth factor, betacellulin and
 CC NTAK. Interaction with these factors induces cell differentiation.
 CC Not activated by EGF, TGF- α , and amphiregulin.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Homodimer or heterodimer with each of the other ERBB
 CC receptors (Potential). Interacts with the PDZ domain of the
 CC synrophin SNTB2.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=The 2 isoforms differ functionally in their response to
 CC phorbol ester: Isoform JM-A is processed but not isoform JM-B.
 CC So, they respectively represent cleavable and noncleavable
 CC forms of the receptor. Both isoforms are expressed in the
 CC cerebellum, but only the isoform JM-B is expressed in the
 CC heart;
 CC Name=JM-A;
 CC IsoId=Q15303-1; Sequence=Displayed;
 CC Name=JM-B;
 CC IsoId=Q15303-2; Sequence=VSP_002895;
 CC -1- TISSUE SPECIFICITY: Expressed at highest levels in brain, heart,
 CC kidney, in addition to skeletal muscle, parathyroid, cerebellum,
 CC pituitary, spleen, testis and breast. Lower levels in thymus,

CC lung, salivary gland, and pancreas.
 CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
 CC residue.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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 CC -----
 CC EMBL: L07868; AAB59446.1; -
 CC DR PIR: A47253; A47253.
 CC DR HSP: P11362; 1FGK.
 CC DR Gene: HGNC:3432; ERBB4.
 CC MIM: 600543; -
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0008283; P: cell proliferation; TAS.
 DR GO: GO:0007275; P: development; TAS.
 DR GO: GO:0007048; P: oncogenesis; TAS.
 DR InterPro: IPR000494; EGF_L_domain.
 DR InterPro: IPR006211; Furin_Like.
 DR InterPro: IPR006212; Furin_repeat.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR InterPro: IPR004019; YLP_motif.
 DR Pfam: PF00757; Furin_Like; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF01030; Recep_L_domain; 2.
 DR Pfam: PF02757; YLP; 2.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_Kinase; 1.
 DR SMART: SM00261; Fu_5.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transmembrane; Glycoprotein; Multigene family; Receptor; Signal;
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW Alternative splicing.
 KW ACT_SITE 843
 FT SIGNAL 1 25
 FT CHAIN 26 1308
 FT DOMAIN 26 651
 FT TRANSMEM 652 675
 FT DOMAIN 676 1308
 FT DOMAIN 186 334
 FT DOMAIN 496 633
 FT DOMAIN 718 985
 FT NP_BIND 724 732
 FT BINDING 751 751
 FT ACT_SITE 843
 FT DISULFID 189 197
 FT DISULFID 193 205
 FT DISULFID 213 221
 FT DISULFID 217 229
 FT DISULFID 230 238
 FT DISULFID 234 246
 FT DISULFID 249 258
 FT DISULFID 262 289
 FT DISULFID 293 304
 FT DISULFID 308 323
 FT DISULFID 326 330
 FT DISULFID 303 312
 FT DISULFID 507 520
 FT DISULFID 523 532
 FT DISULFID 536 552
 FT DISULFID 555 569
 FT DISULFID 559 577
 FT DISULFID 580 589
 FT DISULFID 593 614
 FT DISULFID 617 625

FT DISULFID 621 633 BY SIMILARITY.
 FT MOD_RES 1162 1162 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1168 1168 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1258 1258 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 1284 1284 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 181 181 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 253 253 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 358 358 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 410 410 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 473 473 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 548 548 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 576 576 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC...) (POTENTIAL).
 FT VARSPLIC 626 648 NGPTSHDCIYYPWTGSHLPQHA -> IGSSIDCIGLMD
 (in isoform JM-B).
 FT SEQUENCE 1308 AA; 146807 MW; 554AE80985D88761 CRC64;
 FT /FTId=VSP_002895.

Search completed: February 7, 2004, 13:26:46
 Job time: 13 secs

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OM protein - protein search, using sw model

Run on: February 7, 2004, 13:26:19 ; Search time 34 Seconds

(without alignments)
75.898 Million cell updates/sec

Title: US-09-930-125-3

Sequence: 1 EBYLVPQGF 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	367	11	QBR2X1 mus musculu
2	54	100.0	412	4	QBRVVO mus sapien
3	54	100.0	881	11	Q8COB7 mus musculu
4	54	100.0	1259	6	018735 canis famli
5	54	100.0	1259	11	Q8K3P9 ratu mus norv
6	51	94.4	1209	6	Q8M1L8 mus scrofa
7	50	92.6	1209	11	Q9GX70 ratu mus norv
8	47	87.0	1210	11	Q9EP98 mus musculu
9	46	85.2	545	15	Q85468 avian eryth
10	46	85.2	567	15	Q86714 avian rous-
11	46	85.2	729	15	Q86712 avian rous-
12	46	85.2	962	15	Q64895 avian eryth
13	40	74.1	876	2	Q32739 clostridium
14	40	74.1	876	2	Q9KH41 clostridium
15	38	70.4	910	12	Q9Q915 avian adeno
16	37	68.5	75	11	Q88460 mus musculu

17	37	68.5	428	16	Q92BW2	Q92BW2 listeria in
18	37	68.5	428	16	Q8Y797	Q8Y797 listeria mo
19	37	68.5	539	3	Q01143	Q01143 magnaporthe
20	37	68.5	694	5	Q9UB16	Q9UB16 caenorhabdi
21	37	68.5	753	5	Q9XZD4	Q9XZD4 caenorhabdi
22	37	68.5	861	5	Q8ML27	Q8ML27 drosophila
23	37	68.5	1137	13	Q9W6F6	Q9W6F6 gallus gall
24	36	66.7	173	2	Q8GJES	Q8GJES xenorhabdus
25	36	66.7	332	4	Q9HAA2	Q9HAA2 homo sapien
26	36	66.7	332	4	Q9ECY5	Q9ECY5 homo sapien
27	36	66.7	375	4	Q8WVW8	Q8WVW8 homo sapien
28	36	66.7	432	5	Q9VKT8	Q9VKT8 drosophila
29	36	66.7	436	17	Q97Z48	Q97Z48 sulfolobus
30	36	66.7	1730	13	Q8UY77	Q8UY77 xenopus lae
31	36	66.7	2259	11	Q921C2	Q921C2 mus musculu
32	36	66.7	2304	11	Q921C3	Q921C3 mus musculu
33	36	66.7	3906	2	Q8G987	Q8G987 planktothrix
34	35	64.8	209	3	Q94461	Q94461 schizosach
35	35	64.8	322	16	Q8DD55	Q8DD55 vibrio vuln
36	35	64.8	365	16	Q987M5	Q987M5 rhizobium l
37	35	64.8	481	13	Q8JFP7	Q8JFP7 brachydanio
38	35	64.8	516	3	Q9Y7E1	Q9Y7E1 aspergillus
39	35	64.8	666	11	Q91VG9	Q91VG9 mus musculu
40	35	64.8	686	11	Q9WVJ6	Q9WVJ6 ratu mus norv
41	35	64.8	686	11	Q8C217	Q8C217 mus musculu
42	35	64.8	852	2	Q9AM64	Q9AM64 actinobact
43	35	64.8	917	10	Q94C76	Q94C76 arabidopsis
44	35	64.8	1448	5	Q8T683	Q8T683 dictyostell
45	35	64.8	2269	4	Q96QG9	Q96QG9 homo sapien

ALIGNMENTS

RESULT 1
QBR2X1 PRELIMINARY; PRT; 367 AA.

AC QBR2X1
DT 01-JUN-2002 (TREMURel. 21, Created)
DT 01-JUN-2002 (TREMURel. 21, Last sequence update)
DT 01-MAR-2003 (TREMURel. 23, Last annotation update)

DE Hypothetical 40.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]

RP SEQUENCE FROM N.A.

RA Straube et al. (1992) to the EMBL/GenBank/DBJ databases.

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC027080; AAH27080.1; .

DR InterPro; IPR000719; Prot. Kinase.

DR InterPro; IPR004019; YLP_Motif.

DR Pfam; PF00069; Kinase; 1.

DR Pfam; PF02757; YLP; 2.

DR PRODOM; PD000001; Prot. Kinase; 1.

DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.

KW Hypothetical protein; ATP-binding; Transferase.

KW SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 367;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQGF 10
DB 133 EBYLVPQGF 142

RESULT 2

QBRVVO PRELIMINARY; PRT; 412 AA.
ID QBRVVO
AC QBRVVO;

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypoetical protein.
 GN PP1659.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang Y., Zhou X.M., Zhang P.P., Jiang H.Q., Qin W.X., Zhao X.T.,
 RT Han D.F., Gu J.R.;
 RT "Novel human cDNA clones with function of inhibiting cancer cell
 growth."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF19349; AL55856.1; -
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR004019; YLP_motif.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF02757; YLP; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 KM Hypoetical protein; ATP-binding; Kinase; Transferase;
 KM Tyrosine-protein kinase.
 SQ SEQUENCE 412 AA; 44702 MW; 034397FF3F2D2BC CRC64;

Query Match 100.0%; Score 54; DB 4; Length 412;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 133 EBYLVPQGGF 142

RESULT 3
 Q8OC0E7 PRELIMINARY; PRT; 881 AA.
 ID Q8OC0E7
 AC Q8OC0E7;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE V-erb-b2 erythroblastic leukemia viral oncogene homolog 2
 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=Testis;
 RC MEDLINE=2354683; PubMed=12468851;
 RA the PANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs."
 RL Nature 420:563-573 (2002).
 DR EMBL; AK031542; BAC27442.1; -
 DR NON TER 1
 FT 1
 SQ SEQUENCE 881 AA; 97501 MW; 5D5042BB9F8F0836 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 881;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 647 EBYLVPQGGF 656

RESULT 4
 O18735 PRELIMINARY; PRT; 1259 AA.
 ID O18735
 AC O18735;
 DT 01-JAN-1998 (TReMBLrel. 05, Created)
 DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE ErbB-2.
 OS Canis familiaris (dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Placentalia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yokota H.;
 RT "cDNA cloning of erbB-2 from canine mammary gland."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB008451; BAA23127.1; -
 DR HSP; P11362; IFGK.
 DR InterPro; IPR002048; EGFR_L_domain.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-Like.
 DR InterPro; IPR006212; Furin-repeat.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR004019; YLP_motif.
 DR Pfam; PR00757; Furin-like; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR Pfam; PF02757; YLP; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 3.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KM ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1259 AA; 137989 MW; E37364D9C4ACD46 CRC64;

Query Match 100.0%; Score 54; DB 6; Length 1259;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 1020 EBYLVPQGGF 1029

RESULT 5
 Q8K3F9 PRELIMINARY; PRT; 1259 AA.
 ID Q8K3F9
 AC Q8K3F9;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Neu proto-oncoprotein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BDIX;
 RC Watson P.A., Kim K., Chen K.-S., Gould M.N.;
 RA "Androgen-dependent Mammary Carcinogenesis in Rats Transgenic for the
 RT Neu Proto-Oncogene."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY116182; AAWS0093.1; -
 DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; EF_HAND_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 1259 AA; 139102 MW; B724BD5CC33AE953 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 1259;
 Best Local Similarity 100.0%; Pred. No. 0.068;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
 Db 1025 EBYLVPOQGF 1034

RESULT 6
 ID Q8MIL8 PRELIMINARY; PRT; 1209 AA.
 AC Q8MIL8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Epidermal growth factor receptor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kim J.G., Vallet J.L., Nonneman D., Christenson R.K.;
 RT "Characterization of uterine epidermal growth factor receptor
 expression during the estrous cycle and early pregnancy in pigs."
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY117054; AAM77472.1; -
 DR InterPro; IPR000345; Cyto_heme_bind.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; CYTOCHROME_C; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Receptor; Transferase.
 SQ SEQUENCE 1209 AA; 133531 MW; 268B3FB11536F90F CRC64;

Query Match 94.4%; Score 51; DB 6; Length 1209;
 Best Local Similarity 90.0%; Pred. No. 0.26;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
 Db 1025 EBYLVPOQGF 1034

Db 1014 DEYLVPOQGF 1023

RESULT 7
 ID Q9QX70 PRELIMINARY; PRT; 1209 AA.
 AC Q9QX70;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Epidermal growth factor receptor.
 GN EGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fisher; TISSUE=Liver;
 RX MEDLINE=90258888; PubMed=2342466;
 RA Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.,
 RA Earg H.S.;
 RT "A truncated, secreted form of the epidermal growth factor receptor is
 encoded by an alternatively spliced transcript in normal rat tissue";
 RL Mol. Cell. Biol. 10:2973-2982(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fisher; TISSUE=Liver;
 RA Petch L.A.;
 RL Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.

DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU_3.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1209 AA; 134851 MW; 96FE7F6CC1B7773 CRC64;

Query Match 92.6%; Score 50; DB 11; Length 1209;
 Best Local Similarity 80.0%; Pred. No. 0.41;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EBYLVPOQGF 10
 Db 1015 DEYLVPOQGF 1024

RESULT 8
 ID Q9EP98 PRELIMINARY; PRT; 1210 AA.
 AC Q9EP98;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Epidermal growth factor receptor isoform 1.
 GN EGFR.

OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/101, 129/SvJ, and 129/SvEvTAC;
 RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielson A.J.,
 RA Sinclair C.S., Pearshall R.S., Green P.J., Yee D., Lampfand A.L.,
 RA Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
 RA Maibhe N.J.;
 RT "Comparative genomic sequence analysis and isolation of human and
 RT mouse alternative Egr transcripts encoding truncated receptor
 RT isoforms";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielson A.J.,
 RA Schehl C., Pearshall R.S., Green P.J., Yee D., Lampfand A.L.,
 RA Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
 RA Maibhe N.J.;
 RT "Comparative genomic sequence analysis and isolation of human and
 RT mouse alternative Egr transcripts encoding truncated receptor
 RT isoforms";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF275364; AAG28045.1; JOINED.
 DR EMBL; AF275365; AAG28045.1; JOINED.
 DR EMBL; AF275367; AAG24386.1; -.
 DR HSSP; P11362; 1FGK.
 DR MGD; MGI:95294; Egfr.
 DR InterPro; IPR000345; CytC heme bind.
 DR InterPro; IPR000494; EGFR_L domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF01030; Recep_L domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; Fu; 3.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
 KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 1210 AA; 134840 MW; 62CD021C9E33E18 CRC64;

Query Match 87.0%; Score 47; DB 11; Length 1210;
 Best Local Similarity 80.0%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 1016 DEYLVPOGGF 1025

RESULT 9
 Q85468 PRELIMINARY; PRT; 545 AA.
 AC Q85468;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Avian Erythroblastosis virus (T834) v-erbB gene.
 OS Avian erythroblastosis virus.
 OC Viruses; Retrovirda; Retroviridae; Avian type C retroviruses.
 OC NCBI_TaxID=11861;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=88217326; PubMed=2897102;
 RA Scotting P., Vennartrom B., Jansen M., Graf T., Beug H., Haymann M.J.;
 RT "Common site of mutation in the erbB gene of avian erythroblastosis
 RT virus mutants that are temperature sensitive for transformation";
 RL Oncogene Res. 1:265-278 (1987).
 DR EMBL; X06943; CAA30024.1; -.
 DR HSSP; P11362; 1FGK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 545 AA; 60899 MW; 14DCB9C9A0F8AF4 CRC64;

Query Match 85.2%; Score 46; DB 15; Length 545;
 Best Local Similarity 80.0%; Pred. No. 1.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 439 DEYLVPOGGF 448

RESULT 10
 Q86714 PRELIMINARY; PRT; 567 AA.
 ID Q86714;
 AC Q86714;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE v-erbB protein (Fragment).
 GN v-ERBB.
 OS Avian rous-associated virus type 1.
 OC Viruses; Retrovirda; Retroviridae; Alpharetrovirus.
 OC NCBI_TaxID=11950;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94203659; PubMed=8152791;
 RA Vennartrom B., Raynoscheck C., Jansson L., Doederlein G., Lhotak V.,
 RA Johnson A., Beug H.;
 RT "Retroviral capture of c-erbB proto-oncogene sequences: rapid
 RT evolution of distinct viral genomes carrying mutant v-erbB genes with
 RT different transforming capacities";
 RL Oncogene 9:1307-1320 (1994).
 DR EMBL; S69372; AAC60727.1; -.
 DR HSSP; P11362; 1FGK.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00069; Kinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 FT NON TER 1
 SQ SEQUENCE 567 AA; 63390 MW; C6D9CBA7AD725F1 CRC64;

Query Match 85.2%; Score 46; DB 15; Length 567;
 Best Local Similarity 80.0%; Pred. No. 1.2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EBYLVPQGGF 10
 DB 439 DEYLVPOGGF 448

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RESULT 11
Q86712 PRELIMINARY; PRT; 729 AA.
AC 086712;
DT 01-NOV-1996 (TREMURel. 01, Created)
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
DE Polypeptide.
GN POLYPROTEIN.
OS Avian rous-associated virus type 1.
OC Viruses; Retroviridae; Retrovirinae; Alpharetrovirus.
OX NCBI_TaxID=11950;
RN [1]
RX MEDLINE=94203659; Pubmed=8152791;
RA Vennart B., Raynescheck C., Jansson L., Doederlein G., Lhotak V.,
RA "Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT evolution of distinct viral genomes carrying mutant v-erbB genes with
RT different transforming capacities."
RL Oncogene 9:1307-1320(1994).
DR EMBL; S69372; AAC60725.1; -
DR HSSP; P03322; 1A6S.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR004028; Retro_M.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF02813; Retro_M; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Kinase; transferase; Tyrosine-protein kinase.
KM SEQUENCE 729 AA; 80649 MW; 84D2F6914EFD1D3 CRC64;
SQ
Query Match 85.2%; Score 46; DB 15; Length 729;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 588 DYLVPHQGF 597

RESULT 12
Q64895 PRELIMINARY; PRT; 962 AA.
AC 064895;
DT 01-NOV-1996 (TREMURel. 01, Created)
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
DE Gag/V-erb-A-V-erb-B protein.
GN GAG/V-ERB-A-V-ERB-B.
OS Avian erythroblastosis virus.
OC Viruses; Retroviridae; Retrovirinae; Avian type C retroviruses.
OX NCBI_TaxID=11861;
RN [1]
RX MEDLINE=9020603; Pubmed=1969616;
RA Brunkin A., Jackson J., Bishop J.M., McCarley D.J., Schatzman R.C.;
RT "Six amino acids from the retroviral gene gag greatly enhance the
RT transforming potential of the oncogene v-erb-B."
RL Oncogene 5:15-24(1990).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
DR EMBL; X53209; CAJ36459.1; -
DR EMBL; X53211; CAJ36459.1; JOINED.
DR HSSP; P10828; 2NLL.
DR InterPro; IPR000536; Hormone_rec_1fg.
DR InterPro; IPR000719; Prot_kinase.

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DR InterPro; IPR001723; Stcdhmn_receptor.
DR InterPro; IPR001245; Tyr_Pkinase.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00105; Zf-C4; 1.
DR PRINTS; PR00398; STROHOMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOL1; 1.
DR SMART; SM00219; TyrcK; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; DNA-binding; Kinase; Metal-binding; Nuclear protein;
KM Receptor; Transcription; Transcription regulation; Transferase;
KM Tyrosine-protein kinase; Zinc; Zinc-finger.
SQ SEQUENCE 962 AA; 108320 MW; 3C5ABD791E4E95CE CRC64;

Query Match 85.2%; Score 46; DB 15; Length 962;
Best Local Similarity 80.0%; Pred. No. 2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EYLVPOQGF 10
Db 856 DYLVPHQGF 865

RESULT 13
Q32739 PRELIMINARY; PRT; 876 AA.
AC 032739;
DT 01-JAN-1998 (TREMURel. 05, Created)
DT 01-JAN-1998 (TREMURel. 05, Last sequence update)
DT 01-JUN-2002 (TREMURel. 21, Last annotation update)
DE ADP-riboseyltransferase.
GN ADP-riboseyltransferase.
OS Clostridium difficile.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1496;
RN [1]
RX MEDLINE=97230316; Pubmed=9119480;
RA Perelle S., Gilbert M., Bourlioux P., Cortier G., Popoff M.R.;
RT "Production of a complete binary toxin (actin-specific ADP-
RT ribosyltransferase) by Clostridium difficile CD196."
RL Infect. Immun. 65:1402-1407(1997).
DR EMBL; L76081; AAB67305.1; -
DR HSSP; P13423; IACC.
DR InterPro; IPR003896; Anthrax_toxinB.
DR Pfam; PF03495; Binary_toxB; 1.
DR PRINTS; PR01391; BINARYTOXINB.
KM TRANSFERASE.
SQ SEQUENCE 876 AA; 98797 MW; 25E06E2D45CE2B3B CRC64;

Query Match 74.1%; Score 40; DB 2; Length 876;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EYLVPOQGF 10
Db 696 DYLVPHQGF 704

RESULT 14
Q9KH41 PRELIMINARY; PRT; 876 AA.
ID Q9KH41

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AC 09K41;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CdtB.
 GN CDTB.
 OS Clostridium difficile.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1496;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CCUG 20309;
 RA Chang S.Y., Song K.P.;
 RT "ADP-ribosylating Binary Toxin Genes of Clostridium difficile strain
 CCUG 20309."
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF271719; AAF81761.1; -.
 DR HSPF; P13423; IACC.
 DR InterPro; IPR003896; Anthrax_toxinB.
 DR Pfam; PF03495; Binary_toxB; 1.
 DR PRINTS; PRO1391; BINARYTOXINB.
 SQ SEQUENCE 876 AA; 98793 MW; 366D62F352E745A5 CRC64;

Query Match 74.1%; Score 40; DB 2; Length 876;
 Best Local Similarity 66.7%; Pred. No. 30;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 EBYLVPOQG 10
 DB 696 DYLVPEQGY 704

RESULT 15

09Q915 PRELIMINARY; PRT; 910 AA.
 AC 09Q915;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE 100 kDa protein homolog (Fragment).
 OS Avian adenovirus type 8 (Strain ATCC A-2A) (Fowl adenovirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Aviadenovirus.
 OX NCBI_TaxID=66295;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CFA40;
 RA Johnson M.A., Pooley C.;
 RT "Fowl adenovirus serotype 8 hypervirulent strain CFA40."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF155911; AAF17336.1; -.
 DR InterPro; IPR003381; Adeno_100.
 DR Pfam; PF02438; adeno_100; 1.
 FT NON_TER
 SQ SEQUENCE 910 AA; 102772 MW; EB0BA4227ED2CEC CRC64;

Query Match 70.4%; Score 38; DB 12; Length 910;
 Best Local Similarity 66.7%; Pred. No. 78;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQG 9
 DB 855 EBYLVPEQG 863

Search completed: February 7, 2004, 13:32:06
 Job time : 37 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: February 7, 2004, 13:26:49 ; Search time 22 Seconds
(without alignments)
19.232 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 54

Sequence: 1 EBYLVPOGGF 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	54	100.0	US-08-414-417B-69	Sequence 69, Appl
2	54	100.0	US-08-486-348A-69	Sequence 69, Appl
3	54	100.0	US-08-468-545B-69	Sequence 69, Appl
4	54	100.0	US-08-466-680B-69	Sequence 69, Appl
5	54	100.0	US-08-467-083-69	Sequence 68, Appl
6	54	100.0	US-08-414-417A-68	Sequence 68, Appl
7	54	100.0	US-08-484-438-8	Sequence 8, Appl
8	54	100.0	US-08-486-348A-68	Sequence 68, Appl
9	54	100.0	US-08-625-101-2	Sequence 2, Appl
10	54	100.0	US-08-468-545B-68	Sequence 68, Appl
11	54	100.0	US-08-356-786-2	Sequence 2, Appl
12	54	100.0	US-08-466-680B-68	Sequence 68, Appl
13	54	100.0	US-09-527-487-2	Sequence 12, Appl
14	54	100.0	US-08-128-971B-12	Sequence 12, Appl
15	54	100.0	US-08-484-438-7	Sequence 7, Appl
16	54	100.0	US-08-475-035-4	Sequence 4, Appl
17	54	100.0	US-08-408-604A-69	Sequence 69, Appl
18	54	100.0	US-09-356-818A-2	Sequence 2, Appl
19	54	100.0	US-08-484-438-6	Sequence 6, Appl
20	54	100.0	US-08-247-902A-2	Sequence 2, Appl
21	54	100.0	PCT-US93-10541-2	Sequence 2, Appl
22	54	100.0	PCT-US91-09784-2	Sequence 2, Appl
23	54	100.0	US-08-456-647B-4	Sequence 4, Appl
24	54	100.0	US-08-237-401A-4	Sequence 4, Appl
25	54	100.0	US-08-484-438-4	Sequence 4, Appl
26	54	100.0	US-08-484-438-2	Sequence 2, Appl
27	54	100.0	PCT-US93-01669-56	Sequence 56, Appl

28	36	66.7	209	4	US-09-252-991A-30648	Sequence 30648, A
29	35	64.8	516	4	US-09-215-694-16	Sequence 16, Appl
30	35	64.8	685	5	PCT-US91-09784-4	Sequence 4, Appl
31	34	63.0	182	4	US-09-328-352-8193	Sequence 8193, Ap
32	34	63.0	590	1	US-09-252-991A-19046	Sequence 19046, A
33	33	61.1	9	1	US-08-178-570-63	Sequence 63, Appl
34	33	61.1	9	3	US-08-369-643-63	Sequence 63, Appl
35	33	61.1	9	5	PCT-US95-00147-63	Sequence 63, Appl
36	33	61.1	12	1	US-08-406-192-1	Sequence 1, Appl
37	33	61.1	12	2	US-08-545-151-1	Sequence 1, Appl
38	33	61.1	12	6	US-09-933-12	Sequence 1, Appl
39	33	61.1	27	6	US-09-252-991A-27127	Sequence 27127, A
40	33	61.1	472	2	US-08-821-355A-5	Sequence 5, Appl
41	33	61.1	442	2	US-09-003-687A-5	Sequence 5, Appl
42	33	61.1	442	3	US-09-136-605-5	Sequence 5, Appl
43	33	61.1	491	4	US-09-252-991A-29041	Sequence 29041, A
44	33	61.1	581	2	US-08-724-394A-2	Sequence 2, Appl
45	33	61.1	581	2	US-08-724-394A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-414-417B-69
Sequence 69, Application US/08414417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-414-417B-69
Query Match 100.0%; Score 54; DB 1; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EBYLVPOGGF 10
DB 346 EBYLVPOGGF 355

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RESULT 2
US-08-486-348A-69
; Sequence 69, Application US/08486348A
; Patent No. 5846538
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,348A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-486-348A-69

Query Match          100.0%; Score 54; DB 2; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EBYLVPOQGF 10
        |||||
        346 EBYLVPOQGF 355

RESULT 3
US-08-468-545B-69
; Sequence 69, Application US/08468545B
; Patent No. 5876712
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,545B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-468-545B-69

Query Match          100.0%; Score 54; DB 2; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 580 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-468-545B-69

Query Match          100.0%; Score 54; DB 2; Length 580;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EBYLVPOQGF 10
        |||||
        346 EBYLVPOQGF 355

RESULT 4
US-08-466-680B-69
; Sequence 69, Application US/08466680B
; Patent No. 6075122
; GENERAL INFORMATION:
; APPLICANT: Cheever, Martin A.
; APPLICANT: Disis, Mary L.
; TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
; TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
; TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,680B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Sharkey, Richard G.
; REGISTRATION NUMBER: 32,629
; REFERENCE/DOCKET NUMBER: 920010.448C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 580 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-466-680B-69

Query Match          100.0%; Score 54; DB 3; Length 580;
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Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOGGF 10
Db 346 BEYLVPOGGF 355

RESULT 5

US-08-467-083-68
Sequence 68, Application US/08467083
Patent No. 5726023
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disla, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,083
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/414,417
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836 SEDDANBERRY
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-467-083-68

Query Match 100.0%; Score 54; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOGGF 10
Db 1021 BEYLVPOGGF 1030

RESULT 6

US-08-414-417B-68
Sequence 68, Application US/0841417B
Patent No. 5801005
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disla, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,417B
FILING DATE: 31-MAR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-414-417B-68

Query Match 100.0%; Score 54; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOGGF 10
Db 1021 BEYLVPOGGF 1030

RESULT 7

US-08-484-438-8
Sequence 8, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegal, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl B.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704

FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-438-8

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOGF 10
Db 1021 BEYLVPOGF 1030

RESULT 8
US-08-486-348A-68
Sequence 68, Application US/08486348A
Patent No. 5846538
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486.348A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-486-348A-68

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOGF 10
Db 1021 BEYLVPOGF 1030

RESULT 9
US-08-625-101-2
Sequence 2, Application US/08625101
Patent No. 5869445
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625.101
FILING DATE: 01-APR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-625-101-2

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 BEYLVPOGF 10
Db 1021 BEYLVPOGF 1030

RESULT 10
US-08-468-545B-68
Sequence 68, Application US/08468545B
Patent No. 5876712
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-545B-68

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
DB 1021 EBYLVPOQGF 1030

RESULT 11
US-08-356-786-2
Sequence 2, Application US/08356786
Patent No. 5877305
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
TITLE OF INVENTION: Marker
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Teesta, Hurwitz, & Thibault
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
US-08-466-680B-68

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
DB 1021 EBYLVPOQGF 1030

RESULT 12
US-08-466-680B-68
Sequence 68, Application US/08466680B
Patent No. 6075122
GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.
APPLICANT: Disis, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-68

Query Match 100.0%; Score 54; DB 3; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
DB 1021 EBYLVPOQGF 1030

RESULT 13
US-09-527-487-2
Sequence 2, Application US/09527487

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-356-786-2

Query Match 100.0%; Score 54; DB 2; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
DB 1021 EBYLVPOQGF 1030

Patent No. 6528060
GENERAL INFORMATION:
APPLICANT: Nicolette, Charles
TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
US-09-527-487-2

Query Match 100.0%; Score 54; DB 4; Length 1255;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
DB 1021 EBYLVPOQGF 1030

RESULT 14
US-08-128-971B-12
Sequence 12, Application US/08128971B
Patent No. 5525503
GENERAL INFORMATION:
APPLICANT: Christopher E. Rudd
TITLE OF INVENTION: SIGNAL TRANSDUCTION VIA CD28
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
ZIP: 02110-2804
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/128,971B
FILING DATE: September 28, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraeet
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530/073001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-128-971B-12

Query Match 92.6%; Score 50; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 0.0027;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10

DB 3 DEYLIPOQGF 12

RESULT 15
US-08-484-438-7
Sequence 7, Application US/08484438
Patent No. 5811098
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegfalt, Clay B.
APPLICANT: Hellset m, Ingegerd
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSES: Fennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-438-7

Query Match 92.6%; Score 50; DB 2; Length 1210;
Best Local Similarity 80.0%; Pred. No. 0.36;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EBYLVPOQGF 10
DB 1014 DEYLIPOQGF 1023

Search completed: February 7, 2004, 13:32:39
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 9, 2004, 16:12:17 ; Search time 45 Seconds
(without alignments)
7196.800 Million cell updates/sec

Title: US-09-930-125-2

Perfect score: 6815
Sequence: 1 METALCRMGLLALLPGAA.....TPKGTPTAENPEYGLDVPV 1255

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6304	92.5	1259	6	018735
2	6007.5	88.2	1259	11	08K3P9
3	4216	61.9	881	11	08K3P9
4	3172	46.5	1209	11	09QX70
5	3152.5	46.3	1209	6	08MIL8
6	3143	46.1	1210	11	09BP98
7	2758	40.5	1165	13	09YH40
8	2735.5	40.1	1137	13	09W6F6
9	2326	34.1	1328	13	P79754
10	2209.5	32.4	1305	13	08AW81
11	2043.5	30.0	1433	5	09B1H9
12	2013.5	29.5	1377	5	08MLM0
13	1874.5	27.5	419	4	09UK79
14	1747	25.6	367	11	08R2X1
15	1719	25.2	729	15	086712
16	1717	25.2	567	15	086714

17	1705.5	25.0	412	4	08WYV0	08WYV0 homo sapien
18	1651.5	24.2	962	15	064895	064895 avian eryth
19	1642	24.1	545	15	085468	085468 avian eryth
20	1533.5	22.5	655	11	09WVF5	09WVF5 mus musculus
21	1517.5	22.3	643	11	09ERV6	09ERV6 mus musculus
22	1286	18.9	1193	5	09Y1X8	09Y1X8 ephydracia f
23	1197.5	17.6	1368	5	023821	023821 caenorhabdit
24	1177	17.3	1717	5	026366	026366 echinosoma
25	1155	16.9	527	13	090836	090836 gallus gall
26	1028.5	15.1	478	11	09PSH0	09PSH0 ractus norv
27	971.5	14.3	599	13	09PSH2	09PSH2 gallus gall
28	901	13.2	165	4	014256	014256 homo sapien
29	887	13.0	176	11	0923V5	0923V5 ractus norv
30	814.5	12.0	346	13	P11776	P11776 xiphophorus
31	778	11.4	435	5	08S2M1	08S2M1 dirosophila
32	757	11.1	311	13	099162	099162 xiphophorus
33	754.5	11.1	1362	13	09PVZ4	09PVZ4 xenopus lae
34	737	10.8	1671	5	09N1V5	09N1V5 biophalari
35	734	10.8	331	4	09BDU7	09BDU7 homo sapien
36	723	10.6	149	6	09BG66	09BG66 oryctolagus
37	704.5	10.3	1368	13	08UW85	08UW85 paralicthy
38	700	10.3	1418	13	093457	093457 scophthalmu
39	683.5	10.0	1369	13	08UW86	08UW86 paralicthy
40	680	10.0	1358	13	073798	073798 xenopus lae
41	667.5	9.8	1472	5	09U5A8	09U5A8 bombyx mori
42	659	9.7	1412	13	08UW84	08UW84 paralicthy
43	646.5	9.5	1418	13	08UW83	08UW83 paralicthy
44	646	9.5	1245	13	09YGH8	09YGH8 scophthalmu
45	642	9.4	1371	11	09QVW4	09QVW4 ractus sp.

ALIGNMENTS

RESULT 1
ID 018735 PRELIMINARY; PRT; 1259 AA.
AC 018735;
DT 01-JAN-1998 (TRENBLREL. 05, Created)
DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
DT 01-MAR-2003 (TRENBLREL. 23, Last annotation update)
DE ExB-2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota H.;
RT "cDNA cloning of exB-2 from canine mammary gland."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB008451; BAA23127.1; -
DR HSSP; P11362; IFGK.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR004094; EGFR_L domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR006212; Furin repeat.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR001245; Tyr_Kinase.
DR InterPro; IPR04019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR Pfam; PF02757; YLP_2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SMO0261; FU; 3.
DR SMART; SMO0219; TYRK; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00114; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.

SQ SEQUENCE 1259 AA; 137989 MW; E37364D94CADC46 CRC64;
 Query Match 92.5%; Score 6304; DB 6; Length 1259;
 Best Local Similarity 92.2%; Pred. No. 0;
 Matches 1162; Conservative 38; Mismatches 54; Indels 6; Gaps 2;

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DB 1 MELAMCRWGLLALLPPGAAGTCVCTGDMKRLPASPETHLDMRLHYGCGVQVGNL 60
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QY 121 DPLNNTPTVTGASPGELQRLSLTEILKSGVLIQNPOLCYODTILMKDIFHKNNOLA 180
DB 121 DPLNNTPTVTGASPGELQRLSLTEILKSGVLIQNPOLCYODTILMKDIFHKNNOLA 180
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DB 181 LTLIDTNRSAKCHRCSPKCKSKCWSESSDQSLTRTVCAAGCARGCPPLPTDCHEQC 240
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DB 241 AAGCTGPGHSDCLCLAHNHSIGICELHCPALVTYNTDFESMPNDEGRYTGASCTVACP 300
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DB 301 YNVLSTDVGSCVLCPLNNOEVTABDGTORCEKSKPCARVCYGLGMEHLREVAVTSAN 360
QY 361 IQBPAGCKKIGSLAFPLESPFDGPASNTAPLOEPOLQVETLEITGYLISAMPDLSL 420
DB 361 IQBPAGCKKIGSLAFPLESPFDGPASNTAPLOEPOLQVETLEITGYLISAMPDLSL 420
QY 421 DLSFONLOVRGRILHNGAYSLTQGGISWLGRLSRLBSGSLALHNTHLCFYVTV 480
DB 421 DLSFONLOVRGRILHNGAYSLTQGGISWLGRLSRLBSGSLALHNTHLCFYVTV 480
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DB 481 PMDQLFRNPHQALHTANRPEDECEVGEGLACHQLCARGHCGPPTQCVCNCSQPLRGEC 540
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DB 541 VEECRVLOGLFREYVNAHCLPCHEPCOPONGSVTCFEPEDQCYACAHYDPPCVARC 600
QY 601 PSQVPELSTVMPIMKPEDEBACOPCINCHSCVDLDDKCPAEORASPLTSTISAVG 660
DB 601 PSQVPELSTVMPIMKPEDEBACOPCINCHSCVDLDDKCPAEORASPLTSTISAVG 660
QY 661 ILLVVLGVVFGILIKRQOKIKRKYTMRLLQETELVEPLTPSGAMPQAQMRILKETEL 720
DB 661 ILLVVLGVVFGILIKRQOKIKRKYTMRLLQETELVEPLTPSGAMPQAQMRILKETEL 720
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DB 721 RKVKVLSGAGFTYKGIWIPDGENVKI PVAIKVLRNTSPKANKELIDEAYVMAVGVSP 780
QY 781 YVSRLLGLCTSTVOLVQLMPYGLLDHVRNRRGLSDOLLAMCMOIAAGMSTLEVR 840
DB 781 YVSRLLGLCTSTVOLVQLMPYGLLDHVRNRRGLSDOLLAMCMOIAAGMSTLEVR 840
QY 841 LVHRDLAARNVLYKSPNHYKITDFTGLARLLDIDETEHADGGKVPKIMMALESILRRFT 900
DB 841 LVHRDLAARNVLYKSPNHYKITDFTGLARLLDIDETEHADGGKVPKIMMALESILRRFT 900
QY 901 HOSDWSYGVTVWEIMLTGAKPYDGI PARBEPDLEKESRLLPDPICITIDVYMIWVKCM 960
DB 901 HOSDWSYGVTVWEIMLTGAKPYDGI PARBEPDLEKESRLLPDPICITIDVYMIWVKCM 960
QY 961 IDSECRPRELVEFSRMAHDBORFVYI QNEDLGAPAPLSTFRSLLEDODMDGLVDA 1020
DB 961 IDSECRPRELVEFSRMAHDBORFVYI QNEDLGAPAPLSTFRSLLEDODMDGLVDA 1020
QY 1021 BEYLVPQGFECPPDPAAGGMVHRRSSSTRSGGDLTGLPSEBEPASPLAPSEG 1080
DB 1021 BEYLVPQGFECPPDPAAGGMVHRRSSSTRSGGDLTGLPSEBEPASPLAPSEG 1080
QY 1081 AGSDVFPDGLGMGAAGLQSLPTHDSPFLQRYSDPVPPLPSEFDGYAALPTCSQPEYV 1140
DB 1081 AGSDVFPDGLGMGAAGLQSLPTHDSPFLQRYSDPVPPLPSEFDGYAALPTCSQPEYV 1140
QY 1141 NOPDVRQPPSPRPGPLPAAPAGATLER-----PKTLSPKNGVVKQVFAFGAVENPE 1195
DB 1141 NOPDVRQPPSPRPGPLPAAPAGATLER-----PKTLSPKNGVVKQVFAFGAVENPE 1195
QY 1196 YLTFPGAGAPQHPHPAPPAFDNLVYWDODPPERGAPPSYTFKGTPTAENBEYLGLDVPV 1255
DB 1196 YLTFPGAGAPQHPHPAPPAFDNLVYWDODPPERGAPPSYTFKGTPTAENBEYLGLDVPV 1255
QY 1259 YLABRGAAPQHPHPAPPAFDNLVYWDODPPERGAPPSYTFKGTPTAENBEYLGLDVPV 1259
DB 1259 YLABRGAAPQHPHPAPPAFDNLVYWDODPPERGAPPSYTFKGTPTAENBEYLGLDVPV 1259
  
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RESULT 2
 Q8K3F9 PRELIMINARY; PRT; 1259 AA.
 ID Q8K3F9
 AC Q8K3F9;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE New protooncoprotein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BDIX;
 RA Watson P.A., Kim K., Chen K.-S., Gould M.N.;
 RT "Androgen-Dependent Mammary Carcinogenesis in Rats Transgenic for the
 RT Neu Proto-Oncogene.";
 RL Submitted (May-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY116182; AA050093.1;
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000494; EGFR_L domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; Kinase; 1.
 DR Pfam; PF01030; RecD_L domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR ATP-binding; Transfease.
 SQ SEQUENCE 1259 AA; 139102 MW; B724BD5CC3A953 CRC64;

Query Match 88.2%; Score 6007.5; DB 11; Length 1259;
 Best Local Similarity 88.1%; Pred. No. 0;
 Matches 1106; Conservative 49; Mismatches 100; Indels 1; Gaps 1;

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QY 1 MELALCRWGLLALLPPGAASSTOVCCTGDMKRLPASPETHLDMRLHYGCGVQVGNL 60
DB 4 MELAMCRWGLLALLPPGAAGTCVCTGDMKRLPASPETHLDMRLHYGCGVQVGNL 63
QY 61 ELYTLPTNASISFLQDIOEVGVYLIAHNOVROVPLQRLIRVGTQGFEDNYALAVLNG 120
DB 64 ELYTLPTNASISFLQDIOEVGVYLIAHNOVROVPLQRLIRVGTQGFEDNYALAVLNG 123
QY 121 DPLNNTPTVT GASPGLRELQRLSLTEILKSGVLIQNPOLCYODTILMKDIFHKNNOLA 179
DB 124 DPLNNTPTVTGASPGLRELQRLSLTEILKSGVLIQNPOLCYODTILMKDIFHKNNOLA 183
  
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QY 180 ALTLIDTNRSRACHPCSPMKSGRCWGESEBDCSLTRTWACAGCAACCKGRLPTDCHEQ 239
DB 184 APVIDIDTNRSRACHPCSPACKCKDNHCGESPEDCQILTGITICTSCGACCKGRLPTDCHEQ 243
QY 240 CAAGCGPGRKSDCLACHFNHSGICEAHCPALVTYNTDTESSMNPGRYTFGASCTAC 299
DB 244 CAAGCGPGRKSDCLACHFNHSGICEAHCPALVTYNTDTESSMNPGRYTFGASCTAC 303
QY 300 PNYLSTGVSCCTVCPLEHNOEVAEDGTOCEKSKPCARVCYGLGMEHLREAVATSA 359
DB 304 PNYLSTGVSCCTVCPLEHNOEVAEDGTOCEKSKPCARVCYGLGMEHLREAVATSA 363
QY 360 NIGEPACCKKIFGSLAPLPSFPDPSANTAPLOPEOLQVETLEETGYLYISAMPDSL 419
DB 364 NIGEPACCKKIFGSLAPLPSFPDPSANTAPLOPEOLQVETLEETGYLYISAMPDSL 423
QY 420 PDLSPQNLQVIRGRILHNGAYSLTLOGLSLWGLSLBELSGALILHNTHLCFVHT 479
DB 424 PDLSPQNLQVIRGRILHNGAYSLTLOGLSLWGLSLBELSGALILHNTHLCFVHT 483
QY 480 VPMDOLFRNPHOALLHTANRPEDECVBGLACHOLCARGHGWGPGTQCVNCSQFLRGOE 539
DB 484 VPMDOLFRNPHOALLHTANRPEDECVBGLACHOLCARGHGWGPGTQCVNCSQFLRGOE 543
QY 540 CVEBECRYLQGLPREYVNAHCLPCHPECPONGSVTCFGEADQCVACAHYKOPPCVAR 599
DB 544 CVEBECRYLQGLPREYVNAHCLPCHPECPONGSVTCFGEADQCVACAHYKOPPCVAR 603
QY 600 CPBGVCKDLSYMPWKFPDEBGAOCPCPINCTHSCVDLDDKCPABORASPLTISIAV 659
DB 604 CPBGVCKDLSYMPWKFPDEBGAOCPCPINCTHSCVDLDDKCPABORASPLTISIAV 663
QY 660 GILLVVLGVVFGILLIRBROOKIRKYMRLLOSTELVEPLTPSGAMPNOQMLIKETE 719
DB 664 GILLVVLGVVFGILLIRBROOKIRKYMRLLOSTELVEPLTPSGAMPNOQMLIKETE 723
QY 720 LRKRYLVGSAFGTVYKGIWIPDEBNYKIPALIKYLENTSPKANKEILDEAYMAGVGS 779
DB 724 LRKRYLVGSAFGTVYKGIWIPDEBNYKIPALIKYLENTSPKANKEILDEAYMAGVGS 783
QY 780 PYSRLILGICLTSTVOLVTOLMPYGCILLDHVENRGLSGODLLNMCQIAKMSYLEDV 839
DB 784 PYSRLILGICLTSTVOLVTOLMPYGCILLDHVENRGLSGODLLNMCQIAKMSYLEDV 843
QY 840 RLVHRDLAARNVLYKSPNHVKITDGLARLLDIDETEHADGKVPILKMALESILRRF 899
DB 844 RLVHRDLAARNVLYKSPNHVKITDGLARLLDIDETEHADGKVPILKMALESILRRF 903
QY 900 THOSDVSYGTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPICTIDVYIMVYK 959
DB 904 THOSDVSYGTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPICTIDVYIMVYK 963
QY 960 MIDSECPREELVSEFSRMARDPQRFVIONEDLGPASPLDSTFYNSLLEDDMGDLVD 1019
DB 964 MIDSECPREELVSEFSRMARDPQRFVIONEDLGPASPLDSTFYNSLLEDDMGDLVD 1023
QY 1020 AERTLVPOQGFPCDPRAGAGMHHRRSSSTSSGGDLTLGLEPSEBEPASPLAPSE 1079
DB 1024 AERTLVPOQGFPCDPRAGAGMHHRRSSSTSSGGDLTLGLEPSEBEPASPLAPSE 1083
QY 1080 GAGSDVDGDLGMAAGLGLSLPTHDSPLGRYSEDPVPLPSETDGVAVPLJCSPOEY 1139
DB 1084 GAGSDVDGDLGMAAGLGLSLPTHDSPLGRYSEDPVPLPSETDGVAVPLJCSPOEY 1143
QY 1140 VNOBVPAPPSPREGGLPAARPAAGATLERPKTSLPGKNGVVKVAFAGAVENPEYLP 1199
DB 1144 VNOBVPAPPSPREGGLPAARPAAGATLERPKTSLPGKNGVVKVAFAGAVENPEYLP 1203
QY 1200 OGGAAPQHPAPSPAPADNLYMDODPPEBGAAPSTKGTPTANPEYLGDLV 1255
DB 1204 REGTASBPHPAPSPAPADNLYMDODPPEBGAAPSTKGTPTANPEYLGDLV 1259

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RESULT 3
Q8COE7 ID Q8COE7 PRELIMINARY; PRT; 881 AA.
AC Q8COE7;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE V-erb-b2 erythroblastic leukemia viral oncogene homolog 2
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK031542; BAC27442.1; -
FT NON TER
SQ SEQUENCE 881 AA; 97501 MW; 5D5042B89F0836 CRC64;

Query Match 61.9%; Score 4216; DB 11; Length 881;
Best Local Similarity 88.3%; Pred. No. 8.4e-309;
Matches 778; Conservative 39; Mismatches 64; Indels 0; Gaps 0;

QY 375 APLPESFDGDPASNTAPLOPEOLQVETLEETGYLYISAMPDSLPLDLSVFNQVIRGR 434
DB 1 APLPESFDGDPASNTAPLOPEOLQVETLEETGYLYISAMPESFOLDLSVFNQVIRGR 60
QY 435 ILHNGAYSLTLOGLSLWGLSLBELSGALILHNTHLCFVHTVPMDOLFRNPHOALL 494
DB 61 ILHNGAYSLTLOGLSLWGLSLBELSGALILHNTHLCFVHTVPMDOLFRNPHOALL 120
QY 495 HTANRPEDECVBGLACHOLCARGHGWGPGTQCVNCSQFLRGOECVEBECRYLQGLPREY 554
DB 121 HTANRPEDECVBGLACHOLCARGHGWGPGTQCVNCSQFLRGOECVEBECRYLQGLPREY 180
QY 555 VNARHCLPCHPECPONGSVTCFGEADQCVACAHYKOPPCVARCPBGVCKDLSYMPWK 614
DB 181 VNARHCLPCHPECPONGSVTCFGEADQCVACAHYKOPPCVARCPBGVCKDLSYMPWK 240
QY 615 KPDEBGAOCPCPINCTHSCVDLDDKCPABORASPLTISIAVVGILLVVLGVFGIL 674
DB 241 KPDEBGAOCPCPINCTHSCVDLDDKCPABORASPLTISIAVVGILLVVLGVFGIL 300
QY 675 IKRRQKIRRYTWRLLQETLEVEPLTPSGAMPNOQMLIKETELRKVLGSAFGTV 734
DB 301 IKRRQKIRRYTWRLLQETLEVEPLTPSGAMPNOQMLIKETELRKVLGSAFGTV 360
QY 735 YKGIWIPDEBNYKIPALIKYLENTSPKANKEILDEAYMAGVSPYSRLILGICLTSTV 794
DB 361 YKGIWIPDEBNYKIPALIKYLENTSPKANKEILDEAYMAGVSPYSRLILGICLTSTV 420
QY 795 QLVTLMPYGCILLDHVENRGLSGODLLNMCQIAKMSYLEDVRLVHRDLAARNVLYK 854
DB 421 QLVTLMPYGCILLDHVENRGLSGODLLNMCQIAKMSYLEDVRLVHRDLAARNVLYK 480
QY 855 SPNHVKITDGLARLLDIDETEHADGKVPILKMALESILRRFTHOSDVSYGTVWE 914
DB 481 SPNHVKITDGLARLLDIDETEHADGKVPILKMALESILRRFTHOSDVSYGTVWE 540
QY 915 LMFEGAPYDGIIPAREIPDLLEKGERLPQPICTIDVYIMVYK MIDSECPREELVS 974
DB 541 LMFEGAPYDGIIPAREIPDLLEKGERLPQPICTIDVYIMVYK MIDSECPREELVS 600
QY 975 EFSHARDPQRFVIONEDLGPASPLDSTFYNSLLEDDMGDLVDAERTLVPOQGFPCD 1034

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Db 601 EF8BMAPDQRFVIONEDLGPSSPMDSTFYRSLLEDDBDMLDABEYLVPOQGFSPD 660
Qy 1035 PARGAGGVHHRSSSSSTSGGDLTLGLPESEBAPRSLAPSEGAGSDVFDGLMGGA 1094
Db 661 PALGTGTARRRRSSSSARSGGRLTGLBSEBEPSPSLAPSEGAGSDVFDGLMGGA 720
Qy 1095 AKGLQSLPTDPSLQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVRPQSPRE 1154
Db 721 TKGLQSLPHDLSPLOQRYSEDPVPLPSETDGYVAPLTCSPQPEYVNOQDVRPQSPRE 780
Qy 1155 GDLPAAPBAGATLRLPRTLSGKNGVYKDVAPFGAIVENPEYLPDGGAAQPHPPAPFS 1214
Db 781 GPEPPRLPAGATLRLPRTLSGKNGVYKDVAPFGAIVENPEYLPDGGAAQPHPPAPFS 840
Qy 1215 PAFDNLVYMDQDPPERCAPSTFKGTPTAENPEYLGIDVPY 1255
Db 841 PAFDNLVYMDQDPPERCAPSTFKGTPTAENPEYLGIDVPY 881

RESULT 4
090X70 PRELIMINARY; PRT: 1209 AA.
AC 090X70, PRELIMINARY; PRT: 1209 AA.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 13, Last annotation update)
DE Epidermal growth factor receptor.
GN EGFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RX MEDLINE=90258888; PubMed=2342466;
RA Petch L.A., Harris J., Raymond V.W., Blasband A.J., Lee D.C.,
RA Earp H.S.;
RT "A truncated, secreted form of the epidermal growth factor receptor is
RT encoded by an alternatively spliced transcript in normal rat tissue";
RL Mol. Cell. Biol. 10:2973-2982(1990).
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RA Petch L.A.;
RL Submitted (NOV-1991) to the EMBL/Genbank/DBJ databases.
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=Fisher; TISSUE=Liver;
RA Gutteridge K., Dawson T.L., Earp H.S.;
RL Submitted (NOV-1999) to the EMBL/Genbank/DBJ databases.
DR HSP, P11362, 1FGK.
DR InterPro: IPR000494; EGFR_L domain.
DR InterPro: IPR006211; Furin-like.
DR InterPro: IPR006212; Furin repeat.
DR InterPro: IPR000719; Prot. Kinase.
DR InterPro: IPR001245; Tyr_Kinase.
DR Pfam: PF00757; Furin-like; 1.
DR Pfam: PF00069; Kinase; 1.
DR Pfam: PF01030; Recep_L domain; 2.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SM00261; FU_3.
DR SMART: SM00219; TYKIC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
KW ATP-binding; Kinase; Receptor; Tyrosine-protein kinase.
SQ SEQUENCE 1209 AA; 134891 MW; 96FE7F6CC1B773 CRC64;

Query Match 46.5%; Score 3172; DB 11; Length 1209;
Best Local Similarity 50.2%; Pred. No. 6,7e-230;

Matches 644; Conservative 166; Mismatches 348; Indels 124; Gaps 27;
Qy 3 LAALCRGILLALLPAGA-ASTQVCTGTDMLRLPASPETHLDMRLHYOCQVVOGLLE 61
Db 15 LAALCAAG-----GALBEKVCOSTSNRLTQGLTFEDHFLSLQMFNNCEVYLGLE 66
Qy 62 LTYLPTNASLFLQDIOEVQGYLLAHNOVRQVPLQRLIVRGTOLEFEDNYALAVLQNGD 121
Db 67 ITVQRNYDSLTKTIOEVQGYLLAHNTVERLPLENLIQIRGNALYENTYALAVLSN-- 124
Qy 122 PLANNTPVYASGGRLRELQBSLTILKGGVLIQRNPOLCYQDTILMKDIFHQNQLAL 181
Db 125 -----YGTNKTGLRELWRMLQETLIGAVRSNNPILCNMTIQRDVI--QDVFLSN 175
Qy 182 TLIDTNRS-RACHPSMCKSGRCSBSSBDOSLTVTCAGGCA-RCKGPLPTDCHEQ 239
Db 176 MSMDVQRHLTGCKCKDBSCPNSSCMGRGENCQTLTICAQOCSRCKRGSPPDCCINQ 235
Qy 240 CAAGCTGPKASDCLAHFNHSGI CELHCPALVYNTDTFESMNPBGRYTFGASCVTAQ 299
Db 236 CAAGCTGPRSDCLVCHRFDEATCKOTCPMLNPTTYQMDVNPBGKYSFGATCVKCK 295
Qy 300 PNYVLTSDVSCVLVQELHNOEYTABDTCRCKSCRCARVCGLMENHLEAVATVSA 359
Db 296 PNYVLTSDVSCVLVQELHNOEYTABDTCRCKSCRCARVCGLMENHLEAVATVSA 354
Qy 360 NIEPAGCKKIPGSLAFLESFQDPPASNTAPLOPELOVFEETLEETLYLISAMPDSL 419
Db 355 NIEPAGCKKIPGSLAFLESFQDPPASNTAPLOPELOVFEETLEETLYLISAMPDSL 414
Qy 420 PDISVQNLQVIRGRLHNGAYSLTLOGLISWGLRLSLBLSGGLAIHNHTLCEVHT 479
Db 415 TDLHAFENLEIIRGRTKQHQFSLAVVGLNITSLGLSLKXISIDGVDIISGNRLCYANT 474
Qy 480 VPMDOLEPRNHQALLHNPANPEDECVBEGALCQGLCARHGMGSPQCVVCSQFLRQGE 539
Db 475 INMKKLPFTYNQTKTKIMNNABEDCATNHVCPNLCSECGMGEPDVCSCQNVSRRE 534
Qy 540 CVEBCRYLQGLPREYVNAARHLCFCHPECPONGSVTFEGEADOCVAAHYKDPFCVAR 599
Db 535 CVDKCNILBEPREPFENSCICQHPCLQYTNITTGSGPNDICAHVVDGPHCVKT 594
Qy 600 CPSSGVKEDLSYMPIMKPEDEGACQCPINCTHSVDLDDKCPAEPGRASP-LTSLISAV 658
Db 595 CPSSGIMENNNTL-VMKRADANNVCHLCHANCYGCAGPGLKGC--QQPEBKISIAITGI 651
Qy 652 VGLLFTIV-VALGIGLPMRRRLVRRRTLRLLQERELVEPLTPSGEAPQAHRLRIKE 710
Db 659 VGLLFTIV-VALGIGLPMRRRLVRRRTLRLLQERELVEPLTPSGEAPQAHRLRIKE 717
Qy 718 TELRKVYVLSGAGFGTYKGIWI PDGENVKIPVAIKYLRNTSPKANKELIDEAYVMAV 777
Db 711 TERKTIKVLSSGAFYVYKGLMIPBEKVKIPVAIKYLRNTSPKANKELIDEAYVMAV 770
Qy 778 GSPYVSLGICLTSTVQVLTOLMPYGLLDHVRNENGRGLSODLNMCMQIAKMSYLE 837
Db 771 DNHVHVCRLGICLTSTVQVLTOLMPYGLLDHVRNENGRGLSODLNMCMQIAKMSYLE 830
Qy 838 DVRLVHRDLAARVLYKSPNHVKITDPGLARLIDISTEYHADGKVPKIMMALESILRR 897
Db 831 DRLVHRDLAARVLYKSPNHVKITDPGLARLIDISTEYHADGKVPKIMMALESILRR 890
Qy 898 RFTHSDVMSGYTVWELMTFGAKPYDGI PARISIPDLKEGRLPOPPICITIDYMIWVK 957
Db 891 IYTHSDVMSGYTVWELMTFGSKPYDGI PARISIPDLKEGRLPOPPICITIDYMIWVK 950
Qy 958 CMWIDSECRPRFELVSEFSRMADPQRFVIO-NEDLGASPLDSTFYRSLLEDDBDQGD 1016
Db 951 CMWIDSECRPRFELVSEFSRMADPQRFVIO-NEDLGASPLDSTFYRSLLEDDBDQGD 1010
Qy 1017 LVDAEYLVPOQGFPCDPAAGAGVHHRSSSTSGGDLTLGLPESEBAPRSLA 1076
Db 1011 LVDAEYLVPOQGF-----NSPST-----SRTPLL 1036

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Qy 1077 PSEBAGSVDFPDGLAMGAAGLQSLPTHDPSFLQYSEDPTVPLPSET--DGYAPLTCG 1134
Db 1037 SBLANSN-----SSTVACINRNGSCRVKEDAPLQRYSSDPTSVLTEDIDDTFL----- 1086
Qy 1135 POPEVNOQDVPRPQPPSPREBGLPAPAPAGATL-----ERPRTLSPGKNGVVKDVFACG 1189
Db 1087 PVEPYINO-----SVP-KRPAGSVQNPVYHNQPLHAPAGDLYHQN--PSHN 1130
Qy 1190 AVENPEYL-TEOGGAAPQPHPPAPFADNLYYWDQ-----DP-----PERGA 1232
Db 1131 AVSNPEYLTNQ-----PTCLSSGPFSSALMIQSGSHQMSLDNDYQDDFPFKAK 1181
Qy 1233 PPSTFKGTPTAENPEYLGADVP 1254
Db 1182 PNCIFKQ-PTAENAEYLRVAP 1202

RESULT 5
Q8M1L8 PRELIMINARY; PRT; 1209 AA.
ID Q8M1L8
AC Q8M1L8;
DT 01-OCT-2002 (TReMBLrel. 22. Created)
DT 01-OCT-2002 (TReMBLrel. 22. Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23. Last annotation update)
DE Epidermal growth factor receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9623;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim J.G., Vallet J.L., Nonneman D., Christenson R.K.;
RT "Characterization of uterine epidermal growth factor receptor
RT expression during the oestrous cycle and early pregnancy in pigs.";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY117054; AAM77472.1; -.
DR InterPro; IPR000345; Cytc_heme_bind.
DR InterPro; IPR000494; EGFR_L_domain.
DR InterPro; IPR006211; Furin-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Set_tmr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 2.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00219; Tyrc; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Receptor; Transferase.
SQ SEQUENCE 1209 AA; 133531 MW; 26883F81B36F90F CRC64;

Query March 46.3%; Score 3152.5; DB 6; Length 1209;
Best Local Similarity 49.7%; Pred. No. 2e-228;
Matches 632; Conservative 178; Mismatches 344; Indels 117; Gaps 23;

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Qy 186 TNRBACHPCSPMCKGSRCKWSESSBDQSLTRTVACAGCA-RCKGPLPTDCHECCAGC 244
Db 181 QSLGSCPKCDPGLCNGSCWAGKEMCKTKRVICAQCSGCRGRSPSDCCHNOCAAGC 240
Qy 245 TGRPHSDCLACLNHNSGICELHCPALVTYNTDPEESNPNEGRTFPCASCTAPAYNL 304
Db 241 TGRPSDCLVCRARRRDEATCKDTCPEPLMLYPTTYQMDVNPGLKYSFPAATCYKCPRYNV 300
Qy 305 STDVSGCTLVCPLNQEVTAEDGTORCEKSCKPCARVCYGLAMEHLRBRVATVSANIOEF 364
Db 301 VTDHSGCYRACSSDSYER-BEDGYRKCKCGPCGCKVNGSIGISFKOTLSINAINIKHF 359
Qy 365 AGCKKIFGSLAFDESEFDGDPASNTAPLQEPOLQVFEETLEETGYLYISAMPDSLPLDSV 424
Db 360 RNTSISGDLHILLPVAFRGDSFTRTPLPDPXELDLTKVKEITGFLLIQAMPENRTGLHA 419
Qy 425 FQNLQVIRGLIHNAGVSLTQIGIGISMLGIRSLRELSSGLALIHNNHLCVHVHPMDQ 484
Db 420 FENLEIIRGRKQHQFSLAVAGLDIASLGRSLKEISDGVIVSGNNLCYANTISWKC 479
Qy 485 LFRNPHOALLHTARPEDECVSEGLACHQLCARGHCMGPGPTQVCNCSQFLRGCEVEBC 544
Db 480 LFGTASQKTKIINRSEKCECAMGHICNPLCSSGECGPERDRDCMSCNFSKXCEVEBC 539
Qy 545 RVLQGLPREYVNAHCLPCHCECPONGSVTCFGEADQVACAHYKDPFCVAPCPSCV 604
Db 540 NVLEGEPRFEYNAECVQCHCECLPQANKVTCWNGRGPDSVCRAHYIDGPHCVTKCPADI 599
Qy 605 KPDLSTNPIWKFPEBEACQPCPNCTHSCVDLDDKGPACQORAPLTSISAVY-GILL 663
Db 600 AGENSTL-IWKFADANVCHLCHPNCCTYCGVPGLEGCAVDRPKLP-SIANGVGGILL 656
Qy 664 VVVGAVGGLIKRROOKIRKTYMRLLQETELVEPLTPSGAMPQAOIRLIKETELRV 723
Db 657 AVVALAGVGLFLRR-HIVRKTRIRLLQERELVEPLTPSEBAPQALIRLIKETEFKV 715
Qy 724 KVLGSAFGTVYKGIWIPDGENVKIPVAIKYLRNTSPKAKEILDEAYVAGVSPYVS 783
Db 716 KVLGSAFGTVYKGLWIPDGEKVIPVAIKYLRNTSPKAKEILDEAYVAGVSPYVS 775
Qy 784 RLIGICLTSTVQVLTQMLPFGCLLDHVRNENRGLSGODLWCMQIANGMYLEVRVLVH 843
Db 776 RLIGICLTSTVQVLTQMLPFGCLLDHVRNENRGLSGODLWCMQIANGMYLEVRVLVH 835
Qy 844 RDLAARVLYKSPNHVITDDEGLARLLDIDETEXHADGKVPYKMALESTLRFRFTOS 903
Db 836 RDLAARVLYKTPQHVKITDDEGLAKLGAEXETHAEGKVPYKMALESTLRHYTHOS 895
Qy 904 DVMSYGVVWELMTFGAKPYDGIARBIPLDLEKGERLPQPPICITIDVYMINVKCMIDS 963
Db 896 DVMSYGVVWELMTFGSKPYDGIARBIPLDLEKGERLPQPPICITIDVYMINVKCMIDA 955
Qy 964 ECRFRFELVSEBSRMAADPQRFVYIQ-NEPLGRASPIDSTFFYSLSLEDDMDGLVDABE 1022
Db 956 DSRKPFRELLIIEFKMARDPQRFVYIQDEDEMHLPSPIDSNFYRALMOEEDMEDVADADE 1015
Qy 1023 YLVPQGFPCDPAPAGAGWVHHHRSSSTSGGGDLTLGLEPSEEARPSPLASEGAG 1082
Db 1016 YLVPQGF-HPSTSRTPPLSSLSATST-----PAVACVDRNG-- 1054
Qy 1083 SDVFDGLMGMAAGLQSLPTHDPSFLQYSEDEPTVPLPSET--DGYAPLTCGPOPEYV 1140
Db 1055 -----QSYPLKESFLQRYSSDPTGALTEDSLDTFL-----PAPEYV 1092
Qy 1141 NOPDVPRPQPPSPREBGLPAPAPAGATL-----ERPRTLSPGKNGVVKDVFACG 1195
Db 1093 NO-----SVP-KRPAGSVQNPVYHNQPLHAPAGDLYHQN--SHSNVAGPE 1136
Qy 1196 YL-TPOGGAAPQPHPPAPFADNLYYWDQ-----DP-----PERGAPSTFK 1238
Db 1137 YLNTFR-----PACINGGLDGPAPFMAQTGSHQINLNDNDYQOAFPPKAKNGICK 1187
Qy 1239 GTPAENPEYL 1249

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Db 1188 G-PAENAEYL 1197

RESULT 6

09EP98 PRELIMINARY; PRT; 1210 AA.
 ID 09EP98
 AC 09EP98;
 DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Epidermal growth factor receptor isoform 1.
 GN Egfr.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C3H/101, 129/SvJ, and 129/SvEvTAC;
 RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielson A.J.,
 RA Sinclair C.S., Pearse R.S., Green P.J., Yee D., Lampland A.L.,
 RA Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
 RA Maibhe N.J.;
 RT "Comparative genomic sequence analysis and isolation of human and
 RT mouse alternative Egfr transcripts encoding truncated receptor
 RT isoforms";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RA Reiter J.L., Threadgill D.W., Eley G.D., Strunk K.E., Danielson A.J.,
 RA Schehl C., Pearse R.S., Green P.J., Yee D., Lampland A.L.,
 RA Balasubramaniam S., Crossley T.O., Magnuson T.R., James C.D.,
 RA Maibhe N.J.;
 RT "Comparative genomic sequence analysis and isolation of human and
 RT mouse alternative Egfr transcripts encoding truncated receptor
 RT isoforms";
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF275366; AAG28045.1;
 DR EMBL; AF275365; AAG28045.1; JOINED.
 DR EMBL; AF275367; AAG24386.1;
 DR HSP; P11362; IFCG.
 DR MCD; MGI:95294; Egfr.
 DR InterPro: IPR000345; CytoC_heme_bind.
 DR InterPro: IPR000494; EGFR_L_domain.
 DR InterPro: IPR006211; Furin-Like.
 DR InterPro: IPR006212; Furin_repeat.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR001245; Tyr_kinase.
 DR Pfam; PF00757; Furin-Like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; Fu; 3.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00190; CYTOCHROME_C_1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KM ATP-binding; Kinase; Receptor; Tyrosine-protein kinase.
 SO SEQUENCE 1210 AA; 134840 MW; 62CD021C9D32E18 CRC64;

Query Match 46.1%; Score 3143; DB 11; Length 1210;
 Best Local Similarity 49.7%; Pred. No. 1e-227;
 Matches 635; Conservative 168; Mismatches 354; Indels 120; Gaps 24;

Cy 11 LLLALLPPGAA--STOVCTGTMKRLPASPETHLDMLHYOGGQVQGNLELYLPTN 68
 Db 14 LTLALCAAGALBERKVCQGTISNRLTQLGTFFDHLISLQRMYNCEVVALNLEITYVRN 73

Qy 69 ASLSFLDIOEVQGYVLIANHVRQVPLQRLIRYRGTOLEFDNTALAVLNGDPLNNTTP 128
 Db 74 YDLSFLKTIQEVAGYVLIANTVERIDPLENQLIRGNALYENTVALATLSN----- 124
 Qy 129 VTGASPGGLRELQRLSTELIKGGVLLQORNPOLCYOPTILMKDI-----FHKNQNALTLI 184
 Db 125 -YGTNRGTLELPRNLOEILIGAVRPSNNILCNMDTQWRDLYOVNFMGMSMDL--- 180
 Qy 185 DYNRSRACHPCSPKCKSRGWSSSESDQSLTRVCAGGCA-RCKGPLPTDCHEQCAAG 243
 Db 181 -QSHSPSCPKDPCSPKSGCKGSEBNCQKLTIKICAGQCHRCGRGRPSQCHNQCAAG 239
 Qy 244 CTGPKHSDCLACHFNHSGICELHCPALVYNTDTFESMPNDEGRYTRGASCVTACPNY 303
 Db 240 CTGPRESDCLVQCFQDEATCKDTCPPMLNPTTYQMDVAVDEGYSGATCVKCPANNY 299
 Qy 304 LSTDVSGCTLVCPHNEVTAEDTQCEKSKCARCYGLMEHLREVAVNTSIOE 363
 Db 300 VYTHGSCVBRACGPDYEV--BEDGIRCKCKCDGCRKVCNGIGGEFDLTSLNNTIKH 358
 Qy 364 FAGCKITFGSLAFPLPESFDCDPAANTAPLOPEQLQVETLEITGYLYISAMPDLPDS 423
 Db 359 FKCTALISGDLHLPAVFKDPSFTRTPEDRELEIKTVAEITGFLIIQAMPDQWTDLH 418
 Qy 424 VFQNLQVIRGRILHNGAVSLTLOGLISWGLRSLRELSGLALIHNTHLCFVHTVWD 483
 Db 419 AFENLEIIRGRTHQGFSLAVVGLNITSLRLSKETISDQDVIIISGNRNLCYANTIMWK 478
 Qy 484 QLFENPHQALHTNRPEDCEVSGGLACHQICARGHCGPPTOCVNSQFLRGEQVEE 543
 Db 479 KLFETPNOKTKIMNRBAKDKAVNHNVCNPSBSCGEPEDVSCQNVSRGECVEK 538
 Qy 544 CRVLOGLPREVYNARHCLPCHPECOPONGSVTCGPEADQCVACAHYDPPFCVACRPSG 603
 Db 539 CNLEGPREFVENSEICQHPCLPQAMNITCGRGDNCICQAHYIDGHCVKTCFAG 598
 Qy 604 VKPDLSTMPYKWFDEBACOPCPINCTHSCVDLDDKCPAEORASPLTSIISAVGILL 663
 Db 599 IMGENNTLV-VKXVADANNVCHLCHANCYCGACGGLQCEVWPSGPKPSIATGVGGL 657
 Qy 664 VYVLGVVFGI-LIRROOKIRKYMRRLOTELVEPLTPSGAMPNQOMHILKTELRLK 722
 Db 658 FIVV-VALGIGLFNRHRIYAKKRLRLQRELEVEPLTPSGEADNHLRLKTEFRK 716
 Qy 723 VKVLGSAFGTVYKGIWIPDGENYKIPVAIKVLRBENTSPKANKETILDEAYVAGVSPV 782
 Db 717 IKVLGSAFGTVYKGIWIPBEXKIKIPVAIKVLRBENTSPKANKETILDEAYVAGVSPV 776
 Qy 783 SRLIGICLSTVQLVTOLMPYGCILLDHVENRGRGLSGDILLNMCQIAKMSYLEVRLV 842
 Db 777 CRLLGICLSTVQLVTOLMPYGCILLDYREKDNIGSYLLNMCQIAKMSYLEVRLV 836
 Qy 843 HRDLAANRVLYKSNHYKITDPGLAKLLIDIDETVHADGCVPIKMMALLESILRRRFTHQ 902
 Db 837 HRDLAANRVLYKTPQHKITDPGLAKLLGAEEKYVHAGGVPIKMMALLESILHRTYHQ 896
 Qy 903 SDVWSYGVTVWELMTFGAKPYDGIIPAREIPLLEKGERLPPICTIDVYIMVYKMMID 962
 Db 897 SDVWSYGVTVWELMTFGSKPYDGIIPASDISILKGERLPPICTIDVYIMVYKMMID 956
 Qy 963 SECPRRRELVSERSMARDPQRFVVIQ-NEDLGPASPLDSTFYRSLLEDMDGLVDAE 1021
 Db 957 ADSAPKRELELIFRSKMARDPQRFVVIQGDGRMHLPSPTDSNFYALMDEEMEDVDVAD 1016
 Qy 1022 EYLVPOGCFPCPDPAFPAAGVNHRRHSSSTRSGGDLTLGLPSEBEAPSPFLAPSEGA 1081
 Db 1017 EYLVPOGCFPCPDPAFPAAGVNHRRHSSSTRSGGDLTLGLPSEBEAPSPFLAPSEGA 1042
 Qy 1082 GSDVFDGDLGMAKGLQSLPTDPSPLQFVSEDPVLPSET--DGVAVPLTCSPOPEY 1139
 Db 1043 TSN-----NSTYACINRNGSCAVKEDAFQRISSDPTGAVTEDNIDADL-----PVPEY 1092
 Qy 1140 VNQPDVAFQPPSPREGLPAAPAGATL-----ERPKTLSPGQGVKVDVAFGAVENP 1194

Db 1093 VNO-----SVP-KRPAGSVONPVYHNOPLHAPGRDLHYON--PHSNAVGNP 1136
Qy 1195 EYL-TPOGGAAPQHPAPFSPAFDNLVYWDQ-----DP-----BERGAPSTF 1237
Db 1137 EYLNTAQ-----PTCLSSGFGNSPALWQKSHQMSLDNPDYQDDFFKPKKPGNIF 1187
Qy 1238 KGTPTAENPEYLGIDVP 1254
Db 1188 KG-PTAENAEYLRVAPP 1203
RESULT 7
QyYH40 PRELIMINARY; PRT, 1165 AA.
ID QYH40
AC QYH40
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
DE Receptor tyrosine kinase proto-oncogene.
GN XMRK.
OS Xiphophorus xiphidium.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OC NCBI_Taxid=8086;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rio Purification;
RX MEDLINE=9824117; PubMed=9582016;
RA Altschuld J., Scharl M., Winkler C., Wellbrock C., Gomez A., Duesch J.,
RT "Activation of the Xmrk proto-oncogene of Xiphophorus by
overexpression and mutational alterations.",
RL Oncogene 16:1691-1690 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Rio Purification;
RX Scharl M.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL, U53471; AAD10500.2; -.
DR HSP, P11362; IFGK.
DR InterPro: IPR000345; CYC_heme_bind.
DR InterPro: IPR000494; EGFR_L_domain.
DR InterPro: IPR006212; Purin-Like.
DR InterPro: IPR006212; Purin_repeat.
DR InterPro: IPR00719; Prot_Kinase.
DR InterPro: IPR01245; Tyr_Kinase.
DR Pfam: PF00757; Purin-Like; 1.
DR Pfam: PF00659; Kinase; 1.
DR Pfam: PF01030; Recep_L_domain; 2.
DR PRINTS: PR00109; TYRKINSE.
DR ProDom: PD000001; Prot_Kinase; 1.
DR SMART: SM00261; FU; 3.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS00190; CYCROM C; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
KW SEQUENCE 1165 AA; 12961 MW; 7F7EE38D871A74E CRC64;
Query Match 40.5%; Score 2758; DB 13; Length 1165;
Best Local Similarity 45.9%; Pred. No. 1e-198;
Matches 584; Conservative 164; Mismatches 384; Indels 140; Gaps 29;

Db 57 VLENLEITTYQENODLSFLOSIOEVGYVLAMNEVSTPLVNLRLRGQVLYEGNFTLL 116
Qy 116 VLNDGDEPLANTTPVTGASPGGLRELQSLTEILKGGVLIQRNPOLCYQDTILMKDIFHK 175
Db 117 VMSNYOK-NPSSP--DYGVGLKQLQSLNTEILSGVKVSHNPLCNVETINMWDIVDK 173
Qy 176 NQOLATLITDITNSRACHPSCPMKSGRCWGESSEDDQSLRTVCAGGC-ARCGPLPTD 234
Db 174 TSNPTNMLIHAERQCKDPCGVNCSWAPRGHCKQFTKLLCAQCNCRKCPKPID 233
Qy 235 CCHROGACGCTGPHSDCLALPHNSGICELHCPALVTYNTDTPFESMPEGRYTFGAS 294
Db 234 CCHROGACGCTGPHSDCLALPHNSGICELHCPALVTYNTDTPFESMPEGRYTFGAS 293
Qy 295 CYTACPNVLTSDVGSCTLVCPILNOEVTAEEDGTORCEKSKPCARVCYGLMEHLREVR 354
Db 294 CVKRCPSNYVYTB-GACVRSQASAGMLEVD-ENGRSKCPGCGVPKVDGIGISLNTI 351
Qy 355 AVTSANIQERAGCKKIFGSLAFLESFDPDPASTAPLOPQLOVETLEITGVLYISA 414
Db 352 AVNSTNGSFNCTKINGDIIINNSFEGDPHYKIGPMDPEHLNLTIVKEITGVLYIMW 411
Qy 415 MPDLPDLSVPONLOVTRGRILHNGAYS-LTIOGLGISWTLRSRLSGSLALHNTHT 473
Db 412 WPEMNTSLVFOBLEITRGTTSRGSFVYVQVSHLOMGLSLKEVSAGNVLIAKTPQ 471
Qy 474 LCFVHTVPMQDLFANPHQALLHTANRPEDCEVGEGLACHOLCARGHCMGPPTQVCNSQ 533
Db 472 LRYASTINMRRLPSESDGSEIDART-----ENQCNNECSDEGCGPPTMCVSLH 524
Qy 534 PLRGQCEVERCVLQGLPREYVNAHCLPCHPECPONGSTTCGPEADQVACHYKDP 593
Db 525 VDRGRGVASCNLQGEPRREAYDGRCVQGEQCECLVDTSLTTCGPGPANSCKAHFDDG 584
Qy 594 PFCVARGSPGVKPDLSMPIMKPEBERGACOPCINCHSCVDDDDKCPAQRASPLTS 653
Db 585 PFCVARGSPGVKPDLSMPIMKPEBERGACOPCINCHSCVDDDDKCPAQRASPLTS 642
Qy 654 IISAVGILLVVVGVVFGILIKRQOKIRKYTRRLQETELVEPLTPSGAMPNQAQR 713
Db 643 AVGLVSLILITVIALIIVLRLRRRK-RRTIRRLQEBELVEPLTPSGAPPAQAFLR 701
Qy 714 ILKETELRKVKVLTGSGAFGVYKGIWIPDGENVKIPVAIKYLRENTSFKANKEIIDNAV 773
Db 702 ILKETELRKVKVLTGSGAFGVYKGIWIPDGENVKIPVAIKYLRENTSFKANKEIIDNAV 761
Qy 774 MAGVSPYVRLLGICITSTVQVLTOLMPYCCLDHRENGRLSGODLMMQOIAQGM 833
Db 762 MASVDHPVCCLLGICITSAVQVLTOLMPYCCLDHRENGRLSGODLMMQOIAQGM 821
Qy 834 SYLEDVRLVHRDLAARVLYKSPNHVKITDGLARLLDIDETEHADGKVPKIMMALES 893
Db 822 NYLEBRHLVHRDLAARVLYKSPNHVKITDGLARLLDIDETEHADGKVPKIMMALES 881
Qy 894 ILRRRTHQSDVSYGVTVWELMTFGAKPYDGIIPARISIPDLBKGRPLPOPICTIDYVM 953
Db 882 ILQWLYTHQSDVSYGVTVWELMTFGAKPYDGIIPARISIPDLBKGRPLPOPICTIDYVM 941
Qy 954 IMVCKMIDSECRPRELVESEFARMADPDRFVIONEDIGPASPILSTFRSLLEDD 1013
Db 942 IILCKMIDSECRPRELVESEFARMADPDRFVIONEDIGPASPILSTFRSLLEDD 998
Qy 1014 MGLDVADEEYLVPOCGFCPPDPAAGAGMVHRRASSTRSGGDLTLGLBSEBEAPRS 1073
Db 999 --DYVDADEYLVPOCGFCPPDPAAGAGMVHRRASSTRSGGDLTLGLBSEBEAPRS 1019
Qy 1074 PLAPSEAGSDVFDGLGMAKAGLSLPTHDPSFLQYSDPTV-PLPSETDGVAPLT 1132
Db 1020 FCIPPNGH-----PYEENSIALRYISDPTONALEKIDG----- 1054
Qy 1133 CSPPPEYVNGPDVAPQ-----PSPRE-----GPLP-AARPAATILBRPKTSLPGKNG 1179
Db 1055 -----EYVNGPSETSSRLSDIYNPNYEDLTDGNGPVSLSQEAETNFSRBYLNTNGNS 1109

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QY 1180 VKDVFAGGAVENPEYLTCGGAAPRPHRPAPSPAFDNLVYWDOPPERGAPSTFKG 1239
D 1110 L-----PLVSSGSMDDPDY-----QAG-----YQAF-----LPQGLALTGGMF 1144
QY 1240 TPTAENPEYIGL 1251
D 1145 LPAENLEYLGL 1156

RESULT 8
ID Q9W6F6 PRELIMINARY; PRT; 1137 AA.
Q9W6F6
AC Q9W6F6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Receptor tyrosine kinase (fragment).
GN ERBB4.
OS Gallus gallus (Chicken).
OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Hindbrain;
RX MEDLINE=99263203; PubMed=10328884;
RA Dixon M., Lumsden A.,
RT "Distribution of neuregulin-1 (nrg1) and erbB4 transcripts in
RL embryonic chick hindbrain.",
RL Mol. Cell. Neurosci. 13:237-258 (1999).
DR HMBL; AF121963; AAD31764.1; -.
DR HSSP; P11362; 1FGK.
DR Interpro; IPR000494; EGFR_L_domain.
DR Interpro; IPR006211; Furin-like.
DR Interpro; IPR006212; Furin repeat.
DR Interpro; IPR000719; Prot_kinase.
DR Interpro; IPR001368; TNFR_c6.
DR Interpro; IPR001245; Tyr_kinase.
DR Interpro; IPR004019; YLP_motif.
DR Pfam; PF00757; Furin-like; 1.
DR Pfam; PF00069; Dkinase; 1.
DR Pfam; PF01030; Recep_L_domain; 1.
DR Pfam; PF02757; YLP; 2.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR SMART; SM00261; FU; 3.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
FT NON TER
SQ SEQUENCE 1137 AA; 127927 MW; 4D616436F87DC84F CRC64;

Query Match 40.1%; Score 2735.5; DB 13; Length 1137;
Best Local Similarity 47.5%; Pred. No. 4.9e-197;
Matches 542; Conservative 172; Mismatches 345; Indels 83; Gaps 25;

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QY 340 RVCYGLMEHLAREAVTSANIOEFAGCKKI FGSIAFLPESFDGDPASNTAPLOPQOV 399
D 180 KACDGIQTSLVSAQIVTSSSNDIKFNCTKINGNLIYLVGHGDPHTHIAINPEKINI 239
QY 400 FETLEETITGLYISANPDSLPLDSVFONLOVYIGRIILNAGYISLTLOGLGISWGLBSLR 459
D 240 FQTVREITGYLNIQSWPENMTDFRVSNNLTIGRALYSGISLILKQOQITLQFQSLK 299
QY 460 ELGSGALAIHNTLCEFTVHTVPMDOLEFRNPHOALHTANRPDECEVGLACHOLCARGH 519
D 300 QISAGNIYITDNNLCTYHTVNTSLFSTPSQKTVIHNRKKAENCTADGAVCNLCSDDG 359
QY 520 CWBPPTQCVNCSQPLRQCEVBECEVYLOGLPREYVNAHCLPCHPEQOP-QNGSVTCFG 578
D 360 CWBPPTQCVNCSQPLRQCEVBECEVYLOGLPREYVNAHCLPCHPEQOP-QNGSVTCFG 578
QY 579 PEADQVACAHYNDPPRCVACRPSGVKRPDLSTYPMIKFPPBEAGCOCPCINCHS CYDLD 638
D 420 FGPDHCTKCFHFPVCVAKCPDGLQANSF--IFRYADEDRCHPCHPCTQGC--- 473
QY 639 DKCSPAEQ-----RASPL-----TSISAVV--GILLVVVGVVFGILIKRQOKIR 683
D 474 -RG-PASHDCIYYPWTRQSTLPQHARTPLIAGYIGLFTIIVMGLFAYVVRKSKIK-K 530
QY 684 KYTRRLLOETELVEPLTPSGAMPNQAQRILKTELKRYKVLGSGAFGVYKGIWIPDG 743
D 531 KRALRRL-ETELVEPLTPSGAMPNQAQRILKTELKRYKVLGSGAFGVYKGIWIPDG 589
QY 744 ENKIPYALIVALENTSPRANKSILDEAYVMAGVSGSYVSRILGICLTSTVQLVQLMPY 803
D 590 EYKIPYALIKILNETTGPKANVFMEDALIMASNDHHLVRLGLVCISPTIQLVQLMPH 649
QY 804 GCLLDHYRENRGRIGSODLNMCMQAKGMSYLEDEVLYHRDLAARVLYKSPNHVKITD 863
D 650 GCLLDHYRENRGRIGSODLNMCMQAKGMSYLEDEVLYHRDLAARVLYKSPNHVKITD 863
QY 864 FGLARLLIDETEVHADGKVPILKMMALISILRRRFTHQSDVMSYGVTWELMTFGAKPY 923
D 710 FGLARLLIDETEVHADGKVPILKMMALISILRRRFTHQSDVMSYGVTWELMTFGAKPY 923
QY 924 DGIPTAREIPLLKGERLPPRPCTIDVYVIMMKCMNIDSECRFRFELVSEFSRMAPD 983
D 770 DGIPTAREIPLLKGERLPPRPCTIDVYVIMMKCMNIDSECRFRFELVSEFSRMAPD 983
QY 984 QRFVVIQND-LGPASPLDSTFYSRLLEDMDGLVDAEYLYVQOQFPCDPAPAGAGM 1042
D 830 QRFVVIQND-LGPASPLDSTFYSRLLEDMDGLVDAEYLYVQOQFPCDPAPAGAGM 1042
QY 1043 VHRHRSSTRSGGDLTLGLPSEBEAPRS--PLAF-SEGAGSDVFDGLGMGAALKGLQ 1099
D 889 IDSNRNGFYVRDGYVALEQGV-PWYRAPGIIIEAVVAGATAEIFEDTCNGTLRKQV 947
QY 1100 SLPTHDPSPLOKRSBPTVPLPS-----ETDGYVAPLTCSPPEYVNOVDVAPQPSF 1152
D 948 ATLAKEDESSYORVADPTVPIPERVIRGELDEDDQVMTPMRKPPTDNLNPEENPFVSRR 1007
QY 1153 REGPLPARPAGATLBRPK-TLSPGKNGVAVDVE-----ARGAVENPEYLTPQCGA 1203
D 1008 KNGDLQ-----VDNPEYHNAENQPKADEYVNEPYLNTANTLENAYL----- 1054
QY 1204 APOPHPPAPSPAFDNLVYWDOPPERGA--PSTFKGTP-----AENPE 1247
D 1055 --KNNLEKAKKAFNDNDYNNHSLPRPSTIQHPYLDGYSTKYFYKQNGRIRPIVAENPE 1112
QY 1248 YL 1249
D 1113 YL 1114

RESULT 9
ID P79754 PRELIMINARY; PRT; 1328 AA.
AC P79754;

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DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Erib3.
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorphia; Acanthopterygii; Percomorphia; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Takifugu.
 NCBI_Taxid=31033;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=9177347; PubMed=10077531;
 RA Gellner K., Brenner S.
 RT "Analysis of 148 kb of genomic DNA around the wnt1 locus of Fugu
 rubripes."
 RL Genome Res. 9:251-258(1999).
 DR EMBL; AF056116; AAC34391.1; -.
 DR HSSP; P11362; IFGK.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-Like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001245; Tyr_Kinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recep_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 3.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
 KM SEQUENCE 1328 AA; 148613 MW; A33303258B647B9 CRC64;
 Query Match 34.1%; Score 2326; DB 13; Length 1328;
 Best Local Similarity 40.7%; Pred. No. 4.5e-166;
 Matches 524; Conservative 154; Mismatches 418; Indels 190; Gaps 31;
 QY 9 WGLLALLLP--GAASV---VCTGTMKRLRSPETHLDMLRYOGGVVQVGNEL 62
 DB 4 WRLILMCVARSRLRASSQTOBAVCPGTQNGLSGSGENQYNLMDRKGEIIMGNIEI 63
 QY 63 TYLPFNASLSPLDIOIOGVYVLIANQVROVPLRLRIVGTOLFEDNYALAVLNDGP 122
 DB 64 TQISNNDPSFLKTRVETGYLIAMNHPOEIPLGQLAVIRGNSLYERRFALSYFLN--- 120
 QY 123 LNTTPVTGASPGGIRELQRLSLTEILKGVLIQRPOLCYODTLLMKDIFHKNNQLALT 182
 DB 121 ----YPLDGG--PSGLNQLGLNLTLEILDGVQIINNKTLRGPWWYMDII-RINDAIE 173
 QY 183 LIDTNRBRACPCSPCKGSRCKGSSSEDQSLRTTVAGGC-ARCKPRLTDCCHESCA 241
 DB 174 IQFNGRGVCH---KSC-GNYCWGPGKDCQILTKTVCAPOCNDRCFCFISPRDCHIECA 229
 QY 242 AGCTGPKHSDCLACLFPHNSGICELCPALVTYNTDPESMPNPREGRYTFGASCYTACPY 301
 DB 230 AGCGKPLDTDFACRLPFDSDGACVPCQQTILYNKQITOMETNPAAKYQSGISICVSCPT 289
 QY 302 NYLSTDVOSCTLVCPRLHNOETABDGTOR-CEKSKPCARVCYGLGMEHLREAVRAYSAN 360
 DB 290 HFV-VDSGSCVVCPRDMEV--ERKSGRQCELGGLCPKVCBGEGAL---QRTVDSN 343
 QY 361 IQBPAGCKKLTIGSLAFLPESPDGASNTAPLPQEPOLQVFTLEITGYLYISAMPDLR 420
 DB 344 IDSFINKTKIGSGSHFLVTGLIGDDPKVVPPLADAKKLEVFRTVREITDILNIOQSPKLN 403
 QY 421 DLSTFQNTQVTRGRLHNGAYSLTLQGLISWLGLRSLREIGSGALAHNHTLCEFTV 480
 DB 404 DLSVPSLSITLQGNLFRFSLMVRITPLTSLGSRSLREISDGSVYISQNHLCYHNTV 463
 QY 481 PWDQLFRNPH-QALHTANRPEDECVGBGLACHQLCARGHGCPGPTQCVNCSQPLRGQ 539

DB 464 NMQLFGRGSRVANSLSNRPMAECVADGRVCDPLCSDSGCMGPGPDCLSCRNYSRGT 523
 QY 540 CVEECRYLQGLPREYVANH-CLCPHECQPNQSVTCFGEADQCVAAHYKPPFCVA 598
 DB 524 CVAGCHNSGIPREFALNVCVACHCECKPQTKASCTGAGNACMACTFRDGPYCMS 583
 QY 599 RCPSGVKPLSYNPIKFPDEBEGACQPCPINCISCVLDLDDKGPACORASPLTISAV 658
 DB 584 SCPAGVA-DEKGLIFKFPNRBGHCPCQHCCTGCGGPGINDC---LEARLTSSGOI 639
 QY 659 VGILLVVLVVF-----GILIKRQOKIRKXTMTMRLLQETLVEPLTSGAMPNQAO 711
 DB 640 TGLAGVPAGLIFCLVLPFLGMLYHRLAIRKAMRRYLESSESFEPLCP-GEKGTIVH 698
 QY 712 MRILKETELRRKRVLSGAGFVYKGIWIPDGENVKIPVALKIVRENTSPYANKELDEA 771
 DB 699 ARILKPSDLKIKPLSGGVGTYSKGFWIPBGEIVKLPVALKITQDSSGRQTFETIDHL 758
 QY 772 YNAGVSPYVSRLLGICLTSTVQVLTQMPYGLLDHVRNRRGLSODLLNMCQIAK 831
 DB 759 LSMGSLDHPYIVRLGICPGTCLQVLTQLSHSGILHEIRQKTSLDPQRLNMCVQIAK 818
 QY 832 GMSYLEQVRLVHRDLAARNLVKSPNNVKITDPEGLALDDIDETRYHADGKVPITGMAL 891
 DB 819 GMYLIEHRVYHKNLAKARNLLKNDYQVQISDYVADLLYPDCKYVSETKTPIKMMAL 878
 QY 892 ESILRRRTQSDVMSGYTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPOPPICTIDV 951
 DB 879 ESILFRRTQSDVMSGYTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPOPPICTIDV 938
 QY 952 YMIWKCMTIDSECRPFRELVSEFSHWARDPQFVVIQNEDLGASPLDSTFYRSLLED 1011
 DB 939 YMWVVKCMIDENIRPFLKELASDFTMARAPRYLVIRMG-----ED 982
 QY 1012 DDMGDVDAERYLVPOGFCPPDPAPAGGVNHRHSSSTRSGGDLTLGLEPSEENAP 1071
 DB 983 SGMESEFL-----RGSRR-----GLLEADLEDEDEE-- 1008
 QY 1072 RSPFLAPSEGASDVFDGDLGNG--AAKGLQSLPTHDPSPIQ-----RYSEDPV 1118
 DB 1009 -----GLGDRFATPSLOPSFSWISPCQINSYMTQLRYD----- 1044
 QY 1119 PLPSETDGYAFLTCSPP-ELYNQ-----PVRPQPSPREGL--PAAR 1161
 DB 1045 -FVNSGGHGYLPMSPSPVDITRQLWYQRELSVRLTPRSARFRSSREALECEDGAO 1103
 QY 1162 PAGATLERPKTSLFGKGVKQVADVAFGGAIVENPEYLTPOGGAAPQHPPPAPSPAFDNL 1221
 DB 1104 CAGIFRYR-----FGSERGN-----FOGG----- 1122
 QY 1222 YMDQPPERGAPESTFKGTPTAENPE 1247
 DB 1123 --QQRKLSSTASSPSSFTMAADEDE 1146
 RESULT 10
 Q8AM81 PRELIMINARY; PRT; 1305 AA.
 AC Q8AM81;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE S1:dz150112.1 (Novel protein similar to Erib3 (v-erb-b erythroblastic
 leukemia viral oncogene homolog, neuro/glioblastoma derived oncogene
 homolog).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Sehra H.;
 RL Submitted (JBC-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL/AL591365; CAD58760.1; -
 SQ SEQUENCE 1305 AA; 145709 MW; D026607B19759224 CRC64;

Query Match 32.4%; Score 2209.5; DB 13; Length 1305;
 Best Local Similarity 39.6%; Pred. No. 2,76-157;
 Matches 511; Conservative 170; Mismatches 418; Indels 193; Gaps 31;

QY VCTGTMDKLLPAPFPHDMLRLKLYGCGVYVGNELTLYPTNASSFLDDIGVGV 84
 DB VCTGTMDKLLPAPFPHDMLRLKLYGCGVYVGNELTLYPTNASSFLDDIGVGV 82
 QY LIANQVROYVLOSLRYGTQLFEDNYALVLDNGDPLNNTTVTGSPG--GLREIOL 142
 DB LIANQVROYVLOSLRYGTQLFEDNYALVLDNGDPLNNTTVTGSPG--GLREIOL 131
 QY 83 LIANQVROYVLOSLRYGTQLFEDNYALVLDNGDPLNNTTVTGSPG--GLREIOL 131
 DB 143 RSLTEILKGGVLLQRPOLCYQDTILMKDIFKNNQLALTLIDNRSBACHPSPMCKGS 202
 QY 132 THLTLEIEGGVQIIONKFLSYAPQINMODIV--KNSGAEVLIIONGPEV--PCHESC-GG 186
 DB 203 KCGSESEDDOSLRTNYCAGGC-ARCKGRLPTDCCHGCAAGCTGPKHSDCLALHFNHS 261
 QY 187 PCWPGMDTQQLTKYVCAQCNVRCFGRSPSCCHNECAGGCTGPLDTDCGACRNFNS 246
 DB 262 GICELCPALVTYNTDIFESMPNDEGRYTFGASCTVACPVNYLSTVGSCTLVCPILNOR 321
 QY 247 GSCVSGCPADIVYNTKFKMEPNNAKYQFGSMCVSHCPHFV--VDSSCVSSCPADIME 305
 DB 322 VTAEDGTQRCCKSPCAVVCYGLMEHLREVAVTSANTOEPACCKIFGSLAPLPSF 381
 QY 306 VD-KTGVRCCKSPCAVVCYGLMEHLREVAVTSANTOEPACCKIFGSLAPLPSF 363
 DB 382 DGDPASNTAPLQVFTLEETITGLYLSAMPDLSPLDSVQNLQVIRGRILHNGAY 441
 QY 364 KGSYNNISALDPKLLKIFNTVRBITDLSQSPHELEDISVSNLATIQGRILYRGYS 423
 DB 442 SLTLOGIGISWLGRLSLRELSGALITHNTLCFVHTVPDQFRPHQALLH----- 495
 QY 424 LVMKLTSLSLGRLSLRELSGALITHNTLCFVHTVPDQFRPHQALLH----- 483
 DB 496 TANRDEEC--VSGG---LACHOLCARGHCWGFPTQVNCOSFLRGQCEVCRVLQ 549
 QY 484 KERRPQRCRLGSGTSSVFLQELQKRN-----MCTRLQHLVAG----- 524
 DB 550 LPRRYVNAHCLPCHRECQPNQSVTCGRPADQVACAHKDPFCYCAPSPGVKDL 609
 QY 525 -----SDECKACAHLDQDPYCVSSCPGEGVQGE-N 552
 DB 610 YMPWKPDEBGAQCPINCTHSCVLDLKDGCRAQBPASPLTISAVVGLLVVLGV 669
 QY 553 GLITTKPRNOKOPCHANC-----LSTHYGVNIVRYRLPVYLVSVICVLASVF 609
 DB 670 VFGLIKRROQKIRKTYRRLLOSTELVEPLTPSGAMENQOMILKTELKXKVLGSG 729
 QY 610 VLSVLYRRSLIRKRAMRYLQSGESPELEP-GEKGVKVAHILRLSELKIKLQSG 668
 DB 730 AFGVYVGIWIPDEBNKIPIVAILKVLRENTSPKANKELIDEAVMAGVSGSYVRLIGIC 789
 QY 669 VFGTVHGIWIPEDYKIPVAILKITIDRTKQFOEITDMLMGSIDHAYIVRIIGIC 728
 DB 790 LSTVQVLTOLMPGCLLDHVRNRRGRGSGODLNMCMQIKAGSYLEDVLYVRDLAAR 849
 QY 729 PGASLQVLTQUSPQSLLEHTRORDNINPQLAMCQIKAGSYLEDVLYVRDLAAR 788
 DB 850 NVLVKSPNRYKITDQGLARLLDIDETEXHADGKVPKIMWLESILRRRFTQSDVSYG 909
 QY 789 NILLKSDLIYQIADYGIADLLYPDDKCYFVFEIKTPIKIMWLESILRRRFTQSDVSYG 848
 DB 910 VTVWELMTFGAKPVDGIPAREIPDLLEKGERLPOPPITIVYIMYKCMWIDSECRPF 969
 QY 849 VTVWELMTFGAKPVDGIPAREIPDLLEKGERLPOPPITIVYIMYKCMWIDSECRPF 908

QY 970 RELVSESRNARDPOREVNIONEDLGPASPLDSTFYNS-----LLEDD-----MGDLV 1018
 DB 909 KELANETFRNARDPHRLVKEBDRAPDSASDETHNQSTEDILGVALBEDDDEVLDAI 968
 QY 1019 DAEYLVQOGFCPPDPAQAGMWHRRSS-----STRSGGDLTLGLEPSEER--APRS 1073
 DB 969 DAEYLVQOGFCPPDPAQAGMWHRRSS-----STRSGGDLTLGLEPSEER--APRS 1019
 QY 1074 PL-----APSGAGS---DVPDGLMGAAKGLQSLPHNDEPLRLRYSEDPVPLPSE 1123
 DB 1020 RLDSACTVSSSSRGRLBLEMNDDESSVQSLRRV-----NHRDSA----- 1061
 QY 1124 TDGVVAPLTCSPQPEYVNPDPVPPSPS-----PREGPLPAARPAAGT 1166
 DB 1062 -----TMSQRDLSLGPETITSTGTQGEEDQNEVYLPFGESPKETILLFT 1106
 QY 1167 LER-----PKTLSPGKGVKQVDFAPFGAVENPELITQGGAAAPPHPPAF----- 1213
 DB 1107 SSRSTLSQKRLSRGHSQDFLE--ANRGAGEYEYMNQ--TLISLH1PGOLKEYNORAPR 1162
 QY 1214 --GPAFNLVYMDQPPERGAPSTFKGTPTA 1243
 DB 1163 NRASFPQGMYSNHRSPSKSSITGSESS 1194

RESULT 11

Q9B1H9
 ID Q9B1H9 PRELIMINARY; PRT; 1433 AA.
 AC Q9B1H9;
 DT 01-JUN-2001 (TREMblrel. 17, Created)
 DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
 DT 01-MAR-2003 (TREMblrel. 23, Last annotation update)
 DE Putative epidermal growth factor receptor (Fragment).
 GN EGFR.
 OS Anopheles gambiae (African malaria mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=7165;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SU4;
 RA Lyscelt G.J.;
 RT "Cloning, expression and localisation of the Anopheles gambiae
 RT epidermal growth factor receptor."
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ01655; CAC35008.1; -
 DR HSBP; F11362; JRGK.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-like.
 DR InterPro; IPR006212; Furin repeat.
 DR InterPro; IPR000719; Prot_Kinase.
 DR InterPro; IPR001245; Tyr_Kinase.
 DR Pfam; PF00757; Furin-like; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF01030; Recept_L_domain; 2.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00261; FU; 7.
 DR SMART; SM00219; TYRKC; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Kinase; Receptor; Tyrosine-protein kinase.
 FT NON TER 1
 SQ SEQUENCE 1433 AA; 159585 MW; E3D9D88967724F07 CRC64;

Query Match 30.0%; Score 2043.5; DB 5; Length 1433;
 Best Local Similarity 32.7%; Pred. No. 9,96-145;
 Matches 473; Conservative 196; Mismatches 393; Indels 385; Gaps 36;

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QY 26 CTGTDMKRLPASPETHLDMKRLH YGCGVVOGULETLPTNASLSFLDIOGVGYVL 85
DB 1 CIGTNGMSVYANREYKMLDRYTCYVDGNLEITWIONITDNLQIIRBTGYVL 60
QY 86 IAHNOVQVPLORIRIYRGTOF-----EDNYALAVLNDGPNLNTTPTVTSAGGGLREL 140
DB 61 ISLYDLPOVILPRLOIRGRITFTFKLNMKEBAYGLFV-----SFSHMTL 104
QY 141 QLASLEILKGVLIORNPOLCYODTILMKDI-FHKNQALATLIDTNRSHAPCSFMC 199
DB 105 ELPLRLILOGSVFPNNYNLCHMKSINMBEILAPQSMGYTNFSPREHVCPCPHSC 164
QY 200 KGSRCWGESSEDCSLTFTVCAGCA--RCKGPLTDCCHQCAAGCTGPHSCLACLH 257
DB 165 EVG-CMEGAGANCORFSLNCSPOCSQGRCPGPRRCCHLFCAGGCTGPTOSDCLACKN 223
QY 258 FMSGIELNCPALVYNTDTFESMNPREGRTFGASCVTNCPNYLSTDVSGCTVCP 317
DB 224 FYDDGVKQECPPMOIYNPTNYFWEPNPDGKAYGATVRCR- EHLKNGACVRCRCPK 282
QY 318 HNGEVLADGTORCEKSKPCARVCYGLGMEHLREVRATSANIOEFAGCKIFGSLAFL 377
DB 283 GKRPQNE-----CVPCKGVCPKTCRGGIVH-----SDNIGNYKDCITLIESLEIL 329
QY 378 PESFDGDPASNT-----APLOPELOVELEITGYLYISAMPDLSPLSVFONLQ 429
DB 330 DQSFDFQOYVYTNPSFGRYIKIDPRLEVPSTYKEITGFINIQAHNFTLTYFRLE 389
QY 430 VIRRIILHNGAY-SLTLQGLGISWLGLSLRELSGLALIHNTLCPVHTVPNDQFRN 488
DB 390 VVGGRQKLENFASVYIVKTSLSKSLRLKRVNVSGLVIIENSLCPEVEDIDMSSEIKS 449
QY 489 PHQALHTANRBECEGEGLAGHOLCARHGMGPGPTQCVNCSQFLRGOSVEBCRYLQ 548
DB 450 SDHEVMOVKNNATRECEBEGMECSQKAGCMGKGPQCECKNVKTKGCLDSCK--- 506
QY 549 GLPREY-VNARHCLPCHPECOPONGSVTCFGRPADQCAVACHYDPPFCVARCP----- 601
DB 507 SLRPLYSVSKTCDQHQEKD-----FCYGPNEIDNCSQNNVQDGRCAVACEPTTKAM 561
QY 602 -----SGVXPULSTYMPKFPD----- 618
DB 562 NGTCINCHKTGCRGPRDTIAPDGLSCDKAIIIGSDAKIERCLMKDESCPDGYSDYVL 621
QY 619 -EEG----- 621
DB 622 QEBEPLKOLSGKAVCRKCHPRCKCTGYFHEQFCQCTGYKGEQCEDECPDYANEE 681
QY 622 -ACQPCPINCT-----HSCVDL-----DD-----KGCBAEQ----- 646
DB 682 TRILPCHQBCRGCHGLDHDHCECNLALFPGDPRDANATTTCVNSCNASHPRYKFRQEA 741
QY 647 -----RASPLTISAVVGLLVVLGVNFGI---LIKRRQOKIRKXTM 687
DB 742 GKISPYCSADSMOGLRIEPTQVYKIVMGSVWALLICVVGIAFLVPSRHKNKDKADAVM 801
QY 688 RLLQETELVEPLPSPGAMPNOAQMRILKTELKRVKYLGSAGRTVYKGIWIPGEVVK 747
DB 802 TMAAGCDSBPPLPSNVGNVLTKRITIKERIRGVLAGAFRVRKGVWMPGESSVK 861
QY 748 IPVALKVLRENTSPKANKEILDEAVYMGVSPYVRLGICTSTVOLVLTOLMAYGCLL 807
DB 862 IPVALKVLMEWSSGSSKEPLEBAYVMSVEHPNLKILAVCMISOMMLITQOLMPLGLL 921
QY 808 DHVENRGLSSODLLNWCQOIAKMSYLEVRLVHRLAARVLYKSPNNHKTIDPGLA 867
DB 922 DYVANNKOKISSKALLNWSIOIARGMAVLEBRLLVHRLAARVLYVQPSCKIVFGLA 981
QY 868 RLLIDDEHYADGGKVPKXMALESILRRFTHOSDVWSGVYTWELMTGAKXYDIP 927
DB 982 KLLPDSBYRPAAGGKMPKIMLALCICHHRRFTSKSDVAFGITTWELTGTGARYEVP 1041
QY 928 AREIPDLLEKGBRLPQPICTIDVYIMVWKMMIDSEGRPRRELVSFESMAADPQRFV 987

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DB 1042 AKQVPELIEIGHKLPQPDICSLDYCILLSCWIDADARPFKOLAETFAEKARDPGRYL 1101
QY 988 VIQNEUDGPASPLDSTFYRSLIEDDMGDLV----- 1018
DB 1102 MI-----FGDKFRRLPSYTNQDKDLIRTLAPVAMAAAAAAGASNVDPSTIA 1152
QY 1019 DABEYLVQOGFFCPDPAFAGAGVHHRRSSSTRSGGDLTLGLEPSEEAPRS----- 1073
DB 1153 ETEDEYLOPKTRPSIMLPGPSA-----VEPS-DEMPKSLRYCK 1188
QY 1074 -PLAP---SEGAGDYVDGDLGMGAAGLQSLPTHDSPLORYSEDPVPLPSETDGYVA 1129
DB 1189 DPLKPDDETGHGKEV-----GVGGIR-----LNLPLDEDDYLM 1222
QY 1130 PLTCSPOEVYNQDVPAPPPSPREGPLPARPAGATLERPKLSPGKNGVGVDFARFG 1189
DB 1223 P-TGOSQ-----NQS-----TPG-----YMDLIGVPA 1243
QY 1190 AVENPEYL-----TPOGAAROPHPAPFAPFADNLYYMDQDPERGAPSTFKGT 1240
DB 1244 SYDNPEYLMGSTQALAGLAGSMG--PHTPP-----PNTPPGM 1280
QY 1241 PTANPES 1247
DB 1281 PTHQHSQ 1287

RESULT 12
Q8BMLMO
AC Q8BMLMO PRELIMINARY; PRT; 1377 AA.
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CG10079-PA.
GN EGFR OR CG10079.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Archopoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amentadides P.G., Scherer S.E., Li P.W., Hoekline R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballaw R.M., Baer A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bokora D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Butts K.C., Buzam D.A., Butler H., Cadieu B., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Duthin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
RA Fowler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,
RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.B., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner B., Venter G., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weinstein J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zheng R.A., Myers B.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*,"
 Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banazon J., An H., Baldwin D., Banazon J., Beeson K.Y., Blaum D.A.,
 RA Carlson J.W., Center A., Chapple M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Doree V., Doup L.E., Doyle C., Dresnek D., Fartan D.,
 RA Ferrera S., Frise E., Galle R.F., Gary N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoekins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Paclob J., Pargae V., Park S., Patel S., Pfeiffer B., Pfeiffer F.,
 RA Proulxnavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome,"
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky J., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale J., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnick P., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome,"
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB003454; AAM70919.1; -
 DR FLYBase: FBgn0003731; Egfr.
 DR InterPro: IPR000345; Cytochrome b.
 DR InterPro: IPR000494; EGFR_L domain.
 DR InterPro: IPR006211; Purin-Like.
 DR InterPro: IPR006212; Purin repeat.
 DR InterPro: IPR00719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00757; Furin-like; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR Pfam: PF01030; Recp_L domain; 2.
 DR PRINTS: PR0109; TYRKINASE.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SMO0261; FU; 7.
 DR SMART: SMO0220; S_TKc; 1.
 DR SMART: SMO0219; Tyrc; 1.
 DR PROSITE: PS00190; CYTOCHROME_C; 3.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 KW ATP-binding; Transferase.
 SQ SEQUENCE 1377 AA; 153601 MW; 38AFAAAB9D5C954 CRC64;

Query Match 29.5%; Score 2013.5; DB 5; Length 1377;
 Best Local Similarity 33.1%; Pred. No. 1.7e-142;

Matches	481;	Conservative	185;	Mismatches	435;	Indels	353;	Gaps	42;
QY	9	WGILLALPPGAAS	-----	QVCTGDMKRLPASPETHLDMLYOGC	53				
Db	21	WVLLILLACASITSSSVNAGVNGNMKVCIGTSRLSPVSKNHHYRNLAIDRYTNC	-----	-----	80				
QY	54	QVQVGNIELTYLT-NASLSFLDIDFQVGYVLIANQVROVLRRLRYGTOLF	-----	-----	108				
Db	81	TYVDGNIELTWLIPNENILDSFLNIREVTSYIILSHVDVKKVFPKLIIRGRTLFSLSV	-----	-----	140				
QY	109	-EDNVALAVDNDPLNNTTPVVGASRGRLRLRLTLILKGVLIQRNPOLCYODTI	-----	-----	167				
Db	141	EEKVALFV-----	-----	-----	184				
QY	168	LMDIDFHKNNQALTLIDTRSRACHPCSPMKSGRCMGESSEDDQSLTRTVACAGCA	-----	-----	225				
Db	185	QNSEIYSNGDAYNDVFTAPERECPKCHSCHTG-CWGGSPKNCQKFSKLTGSPQACG	-----	-----	243				
QY	226	RCKGPLETDCHEQCAAGCTGPRHSDCLAFHNSGICELACPALVTYNTDTESMNP	-----	-----	285				
Db	244	RCYGPXKRECBHFCAGGCTGPTQKCIACKNPFDEGVCKECPMKRYPTTVLETNP	-----	-----	303				
QY	286	EGRYTGASCTVACPVNYLSTDVSGCTLVCLNNOBYTAIDGTORCEKSKRCARVYGL	-----	-----	345				
Db	304	EGRYAGATVCKCP-GHLRDNGACVRS-CPQDMRGK-CPVPCNGPCPKTCRGV	-----	-----	357				
QY	346	GMEHLEVRVAVTSANIOEFAGCKIFGSLAFSPESPDG-DPASNTA-----	-----	-----	397				
Db	358	TVLH-----	-----	-----	409				
QY	398	QVETLEETITGYIYISAMPDLPDLSVFQNLQVIRGILHNGAV-SLTLOGLISWGLR	-----	-----	456				
Db	410	EVSSTVEITGYINIEGTHPOFRLSYRMLRTHIGLOMESMPLAIVSSYSLEMR	-----	-----	469				
QY	457	SLRELSGLALHHNTHLCVHTVPMQDLFRNPHQALHTANREDECVSGSLCHQCA	-----	-----	516				
Db	470	NLKOISSGVVIGNRDLCLVSNTRWPATQCEPQKWNENLRADLCENKGTICSDCN	-----	-----	529				
QY	517	RGHCWGPPTQCVNCSQFLRGOECVEECRYLQGLPREYVNAHGLPCHPECPONGSVTC	-----	-----	576				
Db	530	EDCGWAGTQCLCKNFNFNGTCLADGVIYSNKK-FDNRKTKICHPEER-----	-----	-----	581				
QY	577	FGPADQCAAHYKDPFCVYACP-----	-----	-----	605				
Db	582	NGAGADHCQCVHRDQHCVCSECPKKNYDRGVCRECHATCDCTGPKDTIGIACATTC	-----	-----	641				
QY	606	-----	-----	-----	628				
Db	642	NLAINNDATVKKCLLKDCKPD-GY-FWEYVHPQSGSLKPLAGRAVCRKCHPLCELC	-----	-----	698				
QY	629	-----	-----	-----	634				
Db	699	TNYGYHQCYSKTHYRRQCECTECPADHYTDEORCEPCQHPCECNGCTGPGADDCSC	-----	-----	758				
QY	635	-----	-----	-----	653				
Db	759	RNFPLPDANETGPRVNSTWENCTSKCPLEWHVNVYQYATIGPYCAASPSSKITANDV	-----	-----	818				
QY	654	-----	-----	-----	707				
Db	819	NMFIITIGAVLVPTCILCV--TYICRQKQKAKKEVTKMTALSGCDSSEPLRPSNIGA	-----	-----	876				
QY	708	NQAMRIKETELKLVGLSGAGFGTYKGIWIDGENVKIPVAILKLVRENTSPVANKKI	-----	-----	767				
Db	877	NLCRLIVDAELARKGVLGMGAFGRYKGVWEGEVNKKPVAILKELKSTGASSESEF	-----	-----	936				
QY	768	LDEAVYVAGVSSPYVSLGLCLTSTVQVLTQMLPYGCLLDVHRENRGLSQDILLNCM	-----	-----	827				
Db	937	LREAVYVAVSVHVLKILAVCMSSQMLITQLMPLCLLDVYVNNRDKISSKALLNST	-----	-----	996				
QY	828	QIAGKMSYLEVRLVHMDLAARNTLYKSPNHYKLTDPGCLARLLIDREYVADGKVKVIX	-----	-----	887				
Db	997	QIAGKMSYLEBKRLVHDLAARNTLYKSPNHYKLTDPGCLARLLIDREYVADGKVKVIX	-----	-----	1056				

QY 888 WMALESILRRRTTQSDVWSYGVTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPPIC 947
 DB 1057 WLAECIRNRVFTSKSDVWAGVTIWELTTCGRHENIPANDIPDLIEVGLKLEQPPIC 1116
 QY 948 TIDYIMVWKWMDSECRPRELVSFSPMARDPQPFVITQNDLQ--PASPLDSTFY 1005
 DB 1117 SLDTYCTLLSCMHLDAARPTFKOLTYFAFARADPGRYLAI PGDKFTRLP-----Y 1169
 QY 1006 RSLIEDD---DMGDLVDAEYLVPOQGFPCDPAPGAGMWHRRSSSTRSGGDLTLG 1062
 DB 1170 TSGDEKILRKALPTDSSSELAIEPDDYLOPKAAGPS-----HRTCT----- 1213
 QY 1063 LBPSEEARP-----RSLPABSEGASDVFDG---DLGMAKAGLQSLPHDPSPLOYS 1113
 DB 1214 -----DELPKLNRYCKPSNNKSSGTGDETDSSAIEVGNLR----- 1251
 QY 1114 EDPVPLPSETDGYAPLITCSQPEYVNVQPDVRFQPPRECPPLPAARPAATLERPKTL 1173
 DB 1252 ----LDLPVDEDDYLMF--TCQPGFNNNNIN-----NPNQNMMAVGAAGYM----- 1294
 QY 1174 SPGNQGVVQVFAFGAAYENPEYL-----TPQGAPPOH-----PPP 1211
 DB 1295 -----DLIGVPVSYDNEPEYLLNAQTLGVSSPIPTOTIGLPMGVPGTMEYKVPMP 1345
 QY 1212 AFSP-AEPNLYYWD 1224
 DB 1346 GSEPTSSDHEYYND 1359

RESULT 13

QY 09UK79 PRELIMINARY; PRT; 419 AA.
 ID 09UK79

AC 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 23, Last annotation update)
 DE Herstatin.
 GN HER-2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99415951; PubMed=10485918;
 RA Doherty J.K., Bond C., Jardim A., Adelman J.P., Clinton G.M.;
 RT "The HER-2/neu receptor tyrosine kinase gene encodes a secreted
 RT autoinhibitor."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:10869-10874 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Doherty J.K., Clinton G.M., Adelman J.P., Evans A.J., Hennen W.D.;
 RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF17761; AAD56009.2;
 DR InterPro; IPR000494; EGFR_L_domain.
 DR InterPro; IPR006211; Furin-Like.
 DR InterPro; IPR006212; Furin-repeat.
 DR Pfam; PF00757; Furin-Like; 1.
 DR Pfam; PF01030; Recep_L_domain; 1.
 DR SMART; SM00261; FU; 1.
 SQ SEQUENCE 419 AA; 45472 MW; FECLBB347E2D030C CRC64;

Query Match 27.5%; Score 1874.5; DB 4; Length 419;
 Best Local Similarity 89.6%; Pred. No. 8.9e-133;
 Matches 353; Conservative 5; Mismatches 29; Indels 7; Gaps 2;

QY 1 MELALCWMGLLALLPFGASTQVCTGDMCLRLPASBETHLDMRLHYOCQVQVQNTL 60
 DB 1 MELALCWMGLLALLPFGASTQVCTGDMCLRLPASBETHLDMRLHYOCQVQVQNTL 60
 QY 61 ELTYLPTNASISFLQDIOEVQGYVLIANQVRQVPLQRLRIYRGTLQEDNVALAVLNG 120

DB 61 ELTYLPTNASISFLQDIOEVQGYVLIANQVRQVPLQRLRIYRGTLQEDNVALAVLNG 120
 QY 121 DPLNNTPVTVGASPGGLRELOLRSLTEILKGVLIQRPOLCYODTILMKDIFKNNQLA 180
 DB 121 DPLNNTPVTVGASPGGLRELOLRSLTEILKGVLIQRPOLCYODTILMKDIFKNNQLA 180
 QY 181 LFLIDTNRSRACHQSPMCKSRCKWSSBECOSLTRVYCAAGGACRCKGPLETDCHEC 240
 DB 181 LFLIDTNRSRACHQSPMCKSRCKWSSBECOSLTRVYCAAGGACRCKGPLETDCHEC 240
 QY 241 AAGCTGPHSCLACLPHNSGICELHCPALVTYNTDFESMPNDEGRYTFGASCYTACP 300
 DB 241 AAGCTGPHSCLACLPHNSGICELHCPALVTYNTDFESMPNDEGRYTFGASCYTACP 300
 QY 301 YNYLSTDVGSCTLYCPLHNOEVTAEADGTORCEKSKPCARVYGLGMEHLREAVTSAN 360
 DB 301 YNYLSTDVGSCTLYCPLHNOEVTAEADGTORCEKSKPCARVYGLGMEHLREAVTSAN 360
 QY 361 IQEPAKCKLFGSLAPLPESTFGDPAASNTAPLQ 394
 DB 356 LRMQPG--PAHPVLSFLRPSWDLVSAFYSLPLAP 387

RESULT 14

QY 08R2X1 PRELIMINARY; PRT; 367 AA.
 ID 08R2X1

AC 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical 40.2 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Straubeberg R.;
 RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC027080; AAH27080.1;
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR004019; YLP_motif.
 DR Pfam; PF00069; Pkinase; 1.
 DR Pfam; PF02757; YLP; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 KW Hypothetical protein; ATP-binding; Transferase.
 SQ SEQUENCE 367 AA; 40163 MW; 0BE03395F9E101B0 CRC64;

Query Match 25.6%; Score 1747; DB 11; Length 367;
 Best Local Similarity 88.3%; Pred. No. 3e-123;
 Matches 324; Conservative 11; Mismatches 32; Indels 0; Gaps 0;

QY 889 WMALESILRRRTTQSDVWSYGVTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPPIC 948
 DB 1 WMALESILRRRTTQSDVWSYGVTVWELMTFGAKPYDGIIPAREIPDLLEKGERLPQPPIC 948
 QY 949 IDVYIMVWKWMDSECRPRELVSFSPMARDPQPFVITQNDLQ--PASPLDSTFY 1008
 DB 61 IDVYIMVWKWMDSECRPRELVSFSPMARDPQPFVITQNDLQ--PASPLDSTFY 1008
 QY 1009 LEDDDMDLVDAEYLVPOQGFPCDPAPGAGMWHRRSSSTRSGGDLTLGLEPSEE 1068
 DB 121 LEDDDMDLVDAEYLVPOQGFPCDPAPGAGMWHRRSSSTRSGGDLTLGLEPSEE 1068
 QY 1069 EAPRSPLAPSSGAGSDVFDGDLGMAAGLQSLPHDPSPLORYSDDPVPPLPSETDGY 1128
 DB 181 EPPRSPLAPSSGAGSDVFDGDLGMAAGLQSLPHDPSPLORYSDDPVPPLPSETDGY 1128
 QY 1129 APLTCSQPEYVNVQDVRFQPPRECPPLPAARPAATLERPKTLSPGNQGVVQVFAFG 1188
 DB 241 APLTCSQPEYVNVQDVRFQPPRECPPLPAARPAATLERPKTLSPGNQGVVQVFAFG 1188

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QY 1189 GAVENPEYLTPGGAGAPQHPPEPPAFSPADNLVYWDOPPERGAPSTFKCTPAENPEY 1248
DB 301 GAVENPEYLAPRAGTAQPHSPAPAFADNLVYWDQNSSQGPSTFKCTPAENPEY 360
QY 1249 LGLDVVP 1255
DB 361 LGLDVVP 367

RESULT 15
086712
ID 086712 PRELIMINARY; PRT; 729 AA.
AC 086712;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Polyprotein.
GN POLYPROTEIN.
OS Avian rous-associated virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_Taxid=11950;
RN [1]
RP SEQUENCE FROM N. A.
RX MEDLINE=94203659; Pubmed=8152791;
RA Vennetrom B., Raynscheck C., Jansson L., Doederlein G., Lhotak V.,
RA Johnson A., Beug H.;
RT "Retroviral capture of c-erbB proto-oncogene sequences: rapid
RT evolution of distinct viral genomes carrying mutant v-erbB genes with
RT different transforming capacities.";
RL Oncogene 9:1307-1320(1994).
DR EMBL; S69372; AAC60725.1; -.
DR HSSP; P03322; 1A6S.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR004028; Retro_M.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; D_kinase; 1.
DR Pfam; PF02813; Retro_M; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Kinase; Transferase; Tyrosine-protein kinase.
SQ SEQUENCE 729 AA; 80649 MW; 84D2F6914BFID63 CRC64;

Query Match 25.2%; Score 1719; DB 15; Length 729;
Best Local Similarity 54.8%; Freq. No. 1.1e-120;
Matches 358; Conservative 75; Mismatches 118; Indels 102; Gaps 15;
QY 569 PONGSVTCFGEADQCVACAHYKDPFCVAPCPGKPDLSYMPIMKPPDEGACOPCP 628
DB 141 PBNATRTKTPG--DHCKKCAHFIIDGPHCVKACPAVGLGENDTL--VMKADANAVCOLCHP 197
QY 629 NCTHSCVDLDKGCAPAGORASPLTISAVV-GILLVVLGVVFGILIKRQOKIRKXTM 687
DB 198 NCTRGCKAPGLEGP---NGSKTPSIAGVVGILLCLVVGIGLYLRRR-HIVRKRTL 253
QY 688 RLLQETELVLPPLPSGAMPQAOIKRIKTELKRVKVLGSGAGFTYKGIWIDGENYK 747
DB 254 RRLQERELVLPPLPSGAPNQAHLRIKTEFKKVKVLGSGAGFTYKGIWIDGENYK 313
QY 748 IPVAIKVLENTSPKANKELIDEAVYVMAGVSPYVSRLLGICLTSTVOLVQLMPYGL 807
DB 314 IPVAIKELRENTSPKANKELIDEAVYVMASVNPVCRLLGICLTSTVOLVQLMPYGL 373
QY 808 DHVENRGRGLSGDILLNQCWQIAKMSYLEDEVRLVHRDLAARNVLVSPNHVKITDEGLA 867
DB 374 DYIREHKNONISQYILNMCVQIAKGMNLYEERRLVHRDLAARNVLVKTPOHVKITDFGLA 433
QY 868 RLLDIDETEVADGKVIKMALESLIRRRFTHOSDVWSYGVTWELMTGAKPYDGIP 927
DB 434 KLLGADKEXYHAEQGVKPIKMALESILIRIYTHOSDVWSYGVTWELMTGSKPYDGIP 493

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QY 928 AREIPPLEKGERLPPPICTIDVYIMVCMWIDSECRPRELVESEFARMADPORFV 987
DB 494 ASEISSVLEKGERLPPPICTIDVYIMVCMWIDADSREKPRELVESEFARMADPORFV 553
QY 988 VIO-NEDLGPASPLDSTFTYRSLAEDDMDGLVDAEYLVQOGFPCDPAPAGAGMVRHR 1046
DB 554 VIOGERMHLPSPTDSKFYRTLMREBDMEDIVDAEYLVPHQGF 598
QY 1047 HRSSSTRSGGGDLTLGLPSEBEAPRPL-----APSEGASGVFDGDLGMAKGLQSL 1101
DB 599 -NSPT-----SRPLSSLSATSNMNAIYCID-----RNOQH 631
QY 1102 PTHDPSPLOKYSDDPTVPLPSET--DGYAPLTCSPQPEVYVQDPVAPQPSREGLPA 1159
DB 632 PYVEDSPVOKYSDDPTGNFLESIDDOFL-----PAPEVYVQ--LMPKKPS----- 675
QY 1160 ARPAGATLERPKTLSPGKGVVQDF-----ATCGAVENPEYL 1197
DB 676 -----TAVQONQIYNNISLTAISKLPMSRYQNSHSTAVDNPYL 715

```

Search completed: February 9, 2004, 16:16:45
Job time : 52 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 7, 2004, 13:26:19 ; Search time 41 Seconds
(without alignments)
38.714 Million cell updates/sec

Title: US-09-930-125-3

Perfect score: 54

Sequence: 1 EEXLVPPQGR 10

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	54	100.0	10 23 AA20480	Naturally processed
2	54	100.0	10 23 AA077115	Human Her-2/neu im
3	54	100.0	59 23 AAB21202	Human HER-2/neu pr
4	54	100.0	54 23 AAM51147	Human HER-2/neu pr
5	54	100.0	366 23 AAB21201	Human HER-2/neu pr
6	54	100.0	165 23 AAM51145	Human Her-2/neu on
7	54	100.0	293 23 AAB58875	Breast and ovarian
8	54	100.0	583 23 AAE20483	Human protein for
9	54	100.0	581 23 AAE20481	Human protein for

10	54	100.0	1589 23 AA20484	Human protein for
11	54	100.0	600 23 AA20482	Human protein for
12	54	100.0	712 21 AAB21204	Human HER-2/neu fu
13	54	100.0	712 23 AAM51149	Her-2/neu extracel
14	54	100.0	919 21 AAB21203	Human HER-2/neu fu
15	54	100.0	919 23 AAM51148	Her-2/neu extracel
16	54	100.0	920 23 AAM51152	Mouse Her-2/neu ex
17	54	100.0	926 23 AAM51153	Mouse Her-2/neu ex
18	54	100.0	1900 21 AAB21208	Human HER-2/neu pr
19	54	100.0	1923 23 AAU98923	Human breast cance
20	54	100.0	1955 17 AAW01111	HER-2/neu protein
21	54	100.0	1955 20 AAW92406	Human HER-2/neu on
22	54	100.0	1955 21 AAB21198	Human HER-2/neu pr
23	54	100.0	1955 21 AAY84780	Amino acid sequenc
24	54	100.0	1955 21 AAY92620	Human heregulin 2
25	54	100.0	1255 22 AAB21210	Human tyrosine kin
26	54	100.0	1255 22 AAB85458	Human HER-2/neu pr
27	54	100.0	1255 22 AAG88267	HER2/neu amino aci
28	54	100.0	1255 22 AAB60167	HER2 transgene pla
29	54	100.0	1255 23 AAE26349	Human HER-2 protei
30	54	100.0	1255 23 AAE26366	Human HER2 antigen
31	54	100.0	1255 23 AAB24067	Human Her-2 protei
32	54	100.0	1255 23 AA20479	Human Her-2/neu pr
33	54	100.0	1255 23 AAM51143	Human Her-2/neu on
34	54	100.0	1255 23 AAU77114	Human Her-2/neu po
35	54	100.0	1255 23 AAU74545	Human HER2 (ErbB2)
36	54	100.0	1255 24 ABR47447	Breast cancer asso
37	54	100.0	1255 24 ABR74708	Rat HER-2/neu pro
38	54	100.0	1255 21 AAB21199	Mouse Her-2/neu pr
39	54	100.0	1255 21 AAB21206	Mouse Her-2/neu pr
40	54	100.0	1255 22 AAG2860	Amino acid sequenc
41	54	100.0	1255 23 AAM51151	Rat Her-2/neu onco
42	54	100.0	1255 23 AAM51154	Mouse Her-2/neu on
43	54	100.0	1433 14 AAR39568	Sequence of c-erbB
44	54	100.0	1433 14 AAR44876	Inhibitor of TK of
45	50	92.6	13 16 AAR73983	EGF-R derived pept

ALIGNMENTS

RESULT 1
AA20480 standard; peptide; 10 AA.

ID AA20480 standard; peptide; 10 AA.

AC AA20480;

DT 01-JUN-2002 (first entry)

DE Naturally processed HLA-B*44-restricted epitope of human Her-2/neu.

KW Human; Her-2/Neu protein; immune response; gene therapy; breast cancer;

KW human leukocyte antigen; HLA; vaccine; malignancy; cytotoxic.

OS Homo sapiens.

PN W0200214503-A2

PD 21-FEB-2002.

PE 14-AUG-2001; 2001WO-US41733.

PR 14-AUG-2000; 2000US-225152P.

PR 28-SEP-2000; 2000US-236428P.

PR 21-FEB-2001; 2001US-270520P.

PA (CORI-) CORIYA CORP.

PI Hand-zimmermann S, Cheever MA, Foy TW, Lodes MD, Kalos MD;

PI McNeill PD, Veldick TS;

DR WPI; 2002-280758/32.

PT Novel isolated Her-2/Neu polypeptide composition useful for therapy,
 PT prevention and diagnosis of cancer, preferably breast cancer -
 PS Claim 2; Page 87; 129pp; English.
 XX The invention relates to an isolated Her-2/Neu polypeptide composition
 CC effective for eliciting an immune response. The invention is useful for
 CC eliciting an immune response in a patient, where the patient is human
 CC leukocyte antigen (HLA)-B*44 positive or is affected with breast cancer.
 CC The composition is useful for the therapy and diagnosis of cancer.
 CC Preferably breast cancer, in pharmaceutical compositions, e.g., vaccine
 CC and other compositions for the diagnosis, prevention and treatment of
 CC human malignancies, for stimulating and/or expanding T cells specific for
 CC Her-2/Neu polypeptide and for inhibiting the development of cancer in a
 CC patient. The invention is useful for stimulating a T cell response in a
 CC human patient, as probe or primer for nucleic acid hybridization, to
 CC selectively form duplex molecules with complementary stretches of the
 CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full
 CC length gene from a suitable library, and to direct expression of a
 CC polypeptide in appropriate host cells. The composition is useful in
 CC prophylactic or therapeutic applications and for the treatment of cancer,
 CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-
 CC associated malignancies. The invention is useful in gene therapy. The
 CC present sequence is naturally processed HLA-B*44-restricted epitope of
 CC human Her-2/Neu protein.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEYLVPOQGF 10
 |||||
 1 EEYLVPOQGF 10
 DB 1 EEYLVPOQGF 10
 RESULT 2
 AAU77115
 ID AAU77115 standard; Peptide: 10 AA.
 AC AAU77115;
 DT 05-JUN-2002 (first entry)
 DE Human Her-2/neu immunogenic epitope.
 XX Human; Her-2/neu; cytostatic; haematological malignancy; CML;
 KM acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;
 KM chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;
 KM Hodgkin's lymphoma; T cell therapy.
 XX Homo sapiens.
 OS
 PN WO200213847-A2.
 PD 21-FEB-2002.
 PF 13-AUG-2001; 2001WO-US25408.
 PR 14-AUG-2000; 2000US-0638280.
 PR 28-SEP-2000; 2000US-0675904.
 PA (CORI-) CORIXA CORP.
 PI Galger A, Cheever MA, Hand-zimmermann S;
 DR WPI; 2002-280741/32.
 XX
 PT Inhibiting haematological malignancy development by administering
 PT polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide
 PT encoding the polypeptide, or antigen presenting cells expressing the
 PT polypeptide

XX
 PS Claim 2; Page 49; 74pp; English.
 XX The invention relates to a method for inhibiting development of
 CC haematological malignancy in a patient by administering a polypeptide
 CC comprising an immunogenic portion of Her-2/neu or a polynucleotide
 CC encoding the polypeptide. Antigen presenting cells that express the
 CC protein can also be administered. The sequences are used for inhibiting
 CC development of haematological malignancy such as acute myelogenous
 CC leukaemia (AML), chronic myelogenous leukaemia (CML), chronic lymphocytic
 CC leukaemia (CLL), MDS, myelomas, Hodgkin's lymphoma and non-Hodgkin's
 CC lymphoma. This sequence represents a human Her-2/neu immunogenic epitope.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 54; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEYLVPOQGF 10
 |||||
 1 EEYLVPOQGF 10
 DB 1 EEYLVPOQGF 10
 RESULT 3
 AAB21202
 ID AAB21202 standard; protein: 59 AA.
 AC AAB21202;
 DT 12-JAN-2001 (first entry)
 DE Human HER-2/neu protein phosphorylation domain partial sequence.
 XX Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 KM breast cancer; prostate cancer; ovarian cancer; lung cancer;
 KM colon cancer.
 XX Homo sapiens.
 OS
 PN WO200044899-A1.
 PD 03-AUG-2000.
 PF 28-JUN-2000; 2000WO-US02164.
 PR 29-JAN-1999; 99US-0117976.
 PA (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM.
 PI Cheever MA, Gheysen D;
 DR WPI; 2000-505976/45.
 PT HR-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers -
 XX
 PS Claim 27; Fig 11; 129pp; English.
 XX The present sequence is a preferred portion of the phosphorylation domain
 CC of the HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase
 CC family of receptor-like glycoproteins and shows homology to the epidermal
 CC growth factor receptor (EGFR). It probably plays a part in cell growth
 CC and/or differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu
 CC fusion protein comprising a HER-2/neu extracellular domain fused to a
 CC HER-2/neu phosphorylation domain may be used to treat or prevent cancer
 CC by eliciting or enhancing an immune response to the HER-2/neu protein. It
 CC may be used to treat malignancies such as breast, ovarian, colon, lung
 CC and prostate cancers, and may be used as an antigen to vaccinate against
 CC these neoplasias.

Handwritten signature: P6 X DP
Handwritten signature: J. J. J.

SQ Sequence 59 AA;
 Query Match 100.0%; Score 54; DB 21; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEYLVPOQGF 10
 |||||
 DB 32 EEYLVPOQGF 41
 RESULT 4
 ID AAM51147 standard; Protein; 59 AA.
 XX AAM51147;
 AC AAM51147;
 XX 17-JUN-2002 (first entry)
 DE Human Her-2/neu oncoprotein phosphorylation domain fragment.
 XX Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
 KM tyrosine kinase; receptor; c-erbB2; gene therapy.
 XX Homo sapiens.
 OS
 PN WO200212341-A2.
 XX 14-FEB-2002.
 PD 03-AUG-2001; 2001WO-US24283.
 XX 03-AUG-2001; 2000US-0632507.
 PR 03-AUG-2000; 2000US-0632507.
 XX (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX Cheever MA, Gheyssen D;
 PI WPI; 2002-241743/29.
 DR Her-2/neu fusion protein for treating or preventing cancer by eliciting
 PT or enhancing an immune response to the protein, has Her-2/neu
 PT extracellular domain fused to Her-2/neu intracellular or
 PT phosphorylation domain -
 XX Disclosure; Fig 11; 14pp; English.
 PS
 CC The present sequence is that of a fragment (DeltapD) of the
 CC phosphorylation domain of human Her-2/neu (p185 glycoprotein,
 CC c-erbB2), an oncogenic self-protein and target for anti-cancer
 CC vaccines. The Her-2/neu gene is amplified and p185 is
 CC overexpressed in breast, ovarian, colon, lung and prostate cancer.
 CC Her-2/neu (see AAM51143) is a member of the tyrosine kinase family
 CC of receptor-like glycoproteins. It comprises an extracellular
 CC domain with homology to the epidermal growth factor receptor
 CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal
 CC intracellular domain that also shows homology to EGFR. Its
 CC overexpression correlates with a poor prognosis in breast and
 CC ovarian cancers. The invention provides Her-2/neu fusion
 CC proteins, nucleic acids encoding them, viral vectors, and vaccines
 CC comprising the fusion proteins or nucleic acid molecules. In
 CC preferred fusion proteins, the extracellular domain of a Her-2/neu
 CC protein is fused to a Her-2/neu intracellular domain or
 CC phosphorylation domain (or the DeltapD fragment). An immune
 CC response to Her-2/neu protein is elicited or enhanced by
 CC administering the fusion protein in the form of a vaccine, or by
 CC transfecting cells of an animal *ex vivo* with a nucleic acid
 CC encoding the fusion protein, and delivering the transfected cells
 CC to the animal. The fusion proteins, nucleic acids, and isolated
 CC specific T-cells are useful for inhibiting the development of a
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer
 CC in a patient. T cells that specifically react with a Her-2/neu

CC fusion protein can be used to remove tumour cells from a sample in
 CC order to inhibit the development of cancer in a patient.
 SQ Sequence 59 AA;
 Query Match 100.0%; Score 54; DB 23; Length 59;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEYLVPOQGF 10
 |||||
 DB 32 EEYLVPOQGF 41
 RESULT 5
 ID AAB21201 standard; protein; 266 AA.
 XX AAB21201
 AC AAB21201;
 XX 12-JAN-2001 (first entry)
 DE Human HER-2/neu protein phosphorylation domain.
 XX Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
 KM breast cancer; prostate cancer; ovarian cancer; lung cancer;
 KM colon cancer.
 XX Homo sapiens.
 OS
 PN WO200044899-A1.
 XX 03-AUG-2000.
 PD 28-JAN-2000; 2000WO-US02164.
 XX 29-JAN-1999; 99US-0117976.
 PR (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM.
 XX Cheever MA, Gheyssen D;
 PI WPI; 2000-505976/45.
 DR HER-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers -
 XX Claim 2; Fig 10; 128pp; English.
 PS
 CC The present sequence is the phosphorylation domain of the HER-2/neu
 CC protein. HER-2/neu is a member of the tyrosine kinase family of
 CC receptor-like glycoproteins and shows homology to the epidermal growth
 CC factor receptor (EGFR). It probably plays a part in cell growth and/or
 CC differentiation. The HER-2/neu gene is an oncogene. An HER-2/neu fusion
 CC protein comprising a HER-2/neu extracellular domain fused to a HER-2/neu
 CC phosphorylation domain may be used to treat or prevent cancer by
 CC eliciting or enhancing an immune response to the HER-2/neu protein. It
 CC may be used to treat malignancies such as breast, ovarian, colon, lung
 CC and prostate cancers, and may be used as an antigen to vaccinate against
 CC these neoplasias.
 CC
 SQ Sequence 266 AA;
 Query Match 100.0%; Score 54; DB 21; Length 266;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEYLVPOQGF 10
 |||||
 DB 32 EEYLVPOQGF 41

RESULT 6
ID AAM51146 standard; Protein; 266 AA.
XX
AC AAM51146;
XX
DT 17-JUN-2002 (first entry)
XX
DE Human Her-2/neu oncoprotein phosphorylation domain.
XX
KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
KW tyrosine kinase; receptor; c-erbB2; gene therapy.
XX
OS Homo sapiens.
XX
PN MO200212341-A2.
XX
PD 14-FEB-2002.
XX
PF 03-AUG-2001; 2001MO-US24283.
XX
PR 03-AUG-2000; 2000US-0632507.
XX
PA (CORI-) CORIAX CORP.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PI Cheever MA, Cheyssen D;
PI WPI; 2002-241743/29.
XX
DR Her-2/neu fusion protein for treating or preventing cancer by eliciting
PT or enhancing an immune response to the protein, has Her-2/neu
PT extracellular domain fused to Her-2/neu intracellular or
PT phosphorylation domain -
XX
XX
PS Claim 2; Fig 10; 141pp; English.
XX
XX The present sequence is that of the phosphorylation domain of
CC human Her-2/neu (p185 glycoprotein or c-erbB2), an oncogenic
CC self-protein and target for anti-cancer vaccines. The Her-2/neu
CC gene is amplified and p185 is overexpressed in a variety of cancers,
CC including breast, ovarian, colon, lung and prostate cancer.
CC Her-2/neu (see AAM51143) is a member of the tyrosine kinase family
CC of receptor-like glycoproteins. It comprises an extracellular
CC domain with homology to the epidermal growth factor receptor
CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal
CC intracellular domain that also shows homology to EGFR. Its
CC overexpression correlates with a poor prognosis in breast and
CC ovarian cancers. The invention provides Her-2/neu fusion
CC proteins, nucleic acids encoding them, viral vectors, and vaccines
CC comprising the fusion proteins or nucleic acid molecules. In
CC preferred fusion proteins, the extracellular domain of a Her-2/neu
CC protein is fused to a Her-2/neu intracellular domain or
CC phosphorylation domain (or its DeltapD fragment). An immune
CC response to Her-2/neu protein is elicited or enhanced by
CC administering the fusion protein in the form of a vaccine, or by
CC transfecting cells of an animal *ex vivo* with a nucleic acid
CC encoding the fusion protein, and delivering the transfected cells
CC to the animal. The fusion proteins, nucleic acids, and isolated
CC specific T-cells are useful for inhibiting the development of a
CC cancer, especially breast, ovarian, colon, lung or prostate cancer
CC in a patient. T cells that specifically react with a Her-2/neu
CC fusion protein can be used to remove tumour cells from a sample in
CC order to inhibit the development of cancer in a patient.
XX
SQ Sequence 266 AA;
Query Match 100.0%; Score 54; DB 23; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 32 EBYLVPQGGF 41
RESULT 7
ID AAB58875 standard; Protein; 293 AA.
XX
AC AAB58875;
XX
DT 27-MAR-2001 (first entry)
XX
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 583.
XX
XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neutropid; neuroprotective; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiviral; vulnery; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX
OS Homo sapiens.
XX
PN MO200055173-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000MO-US05881.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
PI WPI; 2000-611515/58.
XX
DR N-PSDB; AAF21778.
XX
XX New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX
XX
PS Claim 11; Page 1019-1020; 1299pp; English.
XX
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC neutropid; neuroprotective; antiviral; antiallergic; hepatotropic;
CC antidiabetic; antiinflammatory; antiviral; vulnery; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and cardiac activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and antagonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergy, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemia; wound healing; neurological diseases such as
CC cerebral ischaemia and epilepsy; and infectious diseases.
XX
SQ Sequence 293 AA;
Query Match 100.0%; Score 54; DB 21; Length 293;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 AAB21204
 ID AAB21204 standard; protein; 712 AA.
 AC AAB21204;
 XX
 DT 12-JAN-2001 (first entry)
 XX
 DE Human HER-2/neu fusion protein.
 XX
 KW Human: HER-2/neu; oncogene; tyrosine kinase; cytosolic; vaccine;
 KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
 KW colon cancer; fusion protein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200044899-A1.
 XX
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000MO-US02164.
 XX
 PR 29-JAN-1999; 99US-0117976.
 XX
 PA (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM.
 XX
 PI Cheever MA, Gheylen D;
 XX
 DR WPI; 2000-505976/45.
 XX
 PT HER-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers -
 XX
 PS Claim 27; Fig 13; 128pp; English.
 XX
 CC The present sequence is a fusion protein comprising the extracellular
 CC domain and a preferred portion of the phosphorylation domain of the human
 CC HER-2/neu protein. HER-2/neu is a member of the tyrosine kinase family of
 CC receptor-like glycoproteins and shows homology to the epidermal growth
 CC factor receptor (EGFR). It probably plays a part in cell growth and/or
 CC differentiation. The HER-2/neu gene is an oncogene. HER-2/neu fusion
 CC proteins may be used to treat or prevent cancer by eliciting or enhancing
 CC an immune response to the HER-2/neu protein. They may be used to treat
 CC malignancies such as breast, ovarian, colon, lung and prostate cancers,
 CC and may be used as an antigen to vaccinate against these neoplasias.
 CC
 XX
 SQ Sequence 712 AA;
 XX
 Query Match 100.0%; Score 54; DB 21; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EBYLVPOQGF 10
 DB 685 EBYLVPOQGF 694
 XX
 RESULT 13
 AAM51149
 ID AAM51149 standard; protein; 712 AA.
 AC AAM51149;
 XX
 DT 17-JUN-2002 (first entry)
 XX
 DE Her-2/neu extracellular domain-delta-phosphorylation domain fusion.
 XX
 KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
 KW tyrosine kinase; receptor; c-erbB2; gene therapy.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..653
 FT /note= "extracellular domain"
 FT Domain 654..712
 FT /note= "phosphorylation domain fragment"
 XX
 PN WO200212341-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 03-AUG-2001; 2001WO-US24283.
 XX
 PR 03-AUG-2000; 2000US-0632507.
 XX
 PA (CORI-) CORIXA CORP.
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 PI Cheever MA, Gheylen D;
 XX
 DR WPI; 2002-241743/29.
 XX
 PT Her-2/neu fusion protein for treating or preventing cancer by eliciting
 PT or enhancing an immune response to the protein, has Her-2/neu
 PT extracellular domain fused to Her-2/neu intracellular or
 PT phosphorylation domain -
 XX
 PS Claim 37; Fig 13; 14pp; English.
 XX
 CC The present sequence is that of a fusion protein between the
 CC extracellular domain and a fragment (DeltaEP) of the phosphorylation
 CC domain of human Her-2/neu (see AAM51143), an oncogenic self-phosphorylating
 CC and target for anti-cancer vaccines. The fusion protein can be
 CC obtained by recombinant DNA methods. Her-2/neu overexpression
 CC correlates with a poor prognosis in breast and ovarian cancers.
 CC The invention provides Her-2/neu fusion proteins, nucleic acids
 CC encoding them, viral vectors, and vaccines comprising the fusion
 CC proteins or nucleic acid molecules. In preferred fusion proteins,
 CC the extracellular domain of Her-2/neu is fused to a Her-2/neu
 CC intracellular domain or phosphorylation domain (or its DeltaEP
 CC fragment). An immune response to Her-2/neu protein is elicited or
 CC enhanced by administering the fusion protein in the form of a vaccine,
 CC or by transfecting cells of an animal ex vivo with a nucleic acid
 CC encoding the fusion protein, and delivering the transfected cells
 CC to the animal. The fusion proteins, nucleic acids, and isolated
 CC specific T-cells are useful for inhibiting the development of a
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer
 CC in a patient. T cells that specifically react with a Her-2/neu
 CC fusion protein can be used to remove tumour cells from a sample in
 CC order to inhibit the development of cancer in a patient.
 CC
 XX
 SQ Sequence 712 AA;
 XX
 Query Match 100.0%; Score 54; DB 23; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EBYLVPOQGF 10
 DB 685 EBYLVPOQGF 694
 XX
 RESULT 14
 AAB21203
 ID AAB21203 standard; protein; 919 AA.
 AC AAB21203;
 XX
 DT 12-JAN-2001 (first entry)
 XX
 DE Human HER-2/neu fusion protein.
 XX

KW Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
KW breast cancer; prostate cancer; ovarian cancer; lung cancer;
KW colon cancer; fusion protein.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX W0200044899-A1.
XX
XX 03-AUG-2000.
XX
XX 28-JAN-2000; 2000WO-US02164.
XX
XX 29-JAN-1999; 99US-0117976.
XX
XX (CORI-) CORIXA CORP.
XX (SMIK) SMITHKLINE BEECHAM.
XX
XX Cheever MA, Gheyssen D;
XX
XX WPI; 2000-505976/45.
XX
XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins
XX useful for vaccinating against breast, ovarian, colon, lung and
XX prostate cancers -
XX
XX Claim 2; Fig 12; 128pp; English.
XX
XX The present sequence is a fusion protein comprising the extracellular
XX domain and the phosphorylation domain of the human HER-2/neu protein.
XX HER-2/neu is a member of the tyrosine kinase family of receptor-like
XX glycoproteins and shows homology to the epidermal growth factor receptor
XX (EGFR). It probably plays a part in cell growth and/or differentiation.
XX The HER-2/neu gene is an oncogene. HER-2/neu fusion proteins may be used
XX to treat or prevent cancer by eliciting or enhancing an immune response
XX to the HER-2/neu protein. They may be used to treat malignancies such as
XX breast, ovarian, colon, lung and prostate cancers, and may be used as an
XX antigen to vaccinate against these neoplasias.
XX
XX Sequence 919 AA;
SQ
Query Match 100.0%; Score 54; DB 23; Length 919;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEYLVPOGGF 10
DB 685 EEYLVPOGGF 694
RESULT 15
ID AAM51148
XX AAM51148 standard; Protein; 919 AA.
XX
XX AAM51148;
XX
XX 17-JUN-2002 (first entry)
XX
XX Her-2/neu extracellular domain-phosphorylation domain fusion.
XX
XX Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;
KW tyrosine kinase; receptor; c-erbB2; gene therapy.
XX
XX Homo sapiens.
XX
XX
XX Key Location/Qualifiers
XX FH 1..553
XX FT /note= "extracellular domain"
XX FT 654..919
XX FT /note= "phosphorylation domain"
XX
XX W0200212341-A2.

PD 14-FEB-2002.
XX
XX 03-AUG-2001; 2001WO-US24283.
XX
XX 03-AUG-2000; 2000US-0632507.
XX
XX
XX (CORI-) CORIXA CORP.
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Cheever MA, Gheyssen D;
XX
XX WPI; 2002-241743/29.
XX
XX Her-2/neu fusion protein for treating or preventing cancer by eliciting
XX or enhancing an immune response to the protein, has Her-2/neu
XX extracellular domain fused to Her-2/neu intracellular or
XX phosphorylation domain -
XX
XX Claim 2; Fig 12; 141pp; English.
XX
XX The present sequence is that of a fusion protein between the
XX extracellular domain and phosphorylation domain of human Her-2/neu
XX (see AAM51143), an oncogenic self-protein and target for anti-cancer
XX vaccines. The fusion protein can be obtained by recombinant DNA
XX methods. Her-2/neu overexpression correlates with a poor prognosis
XX in breast and ovarian cancers. The invention provides Her-2/neu
XX fusion proteins, nucleic acids encoding them, viral vectors, and
XX vaccines comprising the fusion proteins or nucleic acid molecules.
XX In preferred fusion proteins, the extracellular domain of a
XX Her-2/neu protein is fused to a Her-2/neu intracellular domain or
XX phosphorylation domain (or its DeltaCD fragment). An immune
XX response to Her-2/neu protein is elicited or enhanced by
XX administering the fusion protein in the form of a vaccine, or by
XX transfecting cells of an animal *ex vivo* with a nucleic acid
XX encoding the fusion protein, and delivering the transfected cells
XX to the animal. The fusion proteins, nucleic acids, and isolated
XX specific T-cells are useful for inhibiting the development of a
XX cancer, especially breast, ovarian, colon, lung or prostate cancer
XX in a patient. T cells that specifically react with a Her-2/neu
XX fusion protein can be used to remove tumour cells from a sample in
XX order to inhibit the development of cancer in a patient.
XX
XX Sequence 919 AA;
SQ
Query Match 100.0%; Score 54; DB 23; Length 919;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEYLVPOGGF 10
DB 685 EEYLVPOGGF 694
Search completed: February 7, 2004, 13:31:17
Job time : 42 secs